



SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Daggett, Lorrie P.
Ellis, Steven B.
Liaw, Chen W.
Lu, Chin-Chun
- (ii) TITLE OF INVENTION: HUMAN N-METHYL-D-ASPARTATE RECEPTOR
SUBUNITS, DNA ENCODING SAME AND USES THEREFOR
- (iii) NUMBER OF SEQUENCES: 21
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
 - (B) STREET: 444 South Flower Street, Suite 2000
 - (C) CITY: Los Angeles
 - (D) STATE: CA
 - (E) COUNTRY: U.S.A.
 - (F) ZIP: 90071-2921
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE: 20-APR-1994
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/052,449
 - (B) FILING DATE: 20-APR-1993
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Reiter, Stephen E.
 - (B) REGISTRATION NUMBER: 31,192
 - (C) REFERENCE/DOCKET NUMBER: P41 9424
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 619-546-4737
 - (B) TELEFAX: 619-546-9392

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4298 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: both
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 262..3078

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CAAGCCGGGC GTTCGGAGCT GTGCCCCGCC CCGCTTCAGC ACCGCGGACA GCGCCGGCCG	60
CGTGGGGCTG AGCGCCGAGC CCCC CGCAC GCTTCAGCCC CCCTTCCCTC GGCCGACGTC	120
CCGGGACCGC CGCTCCGGGG GAGACG ¹³⁰ GTCCGCAGCC CGCGGGGCCG GGCGAGCGCA	180
GGACGGCCCG GAAGCCCCGC GGGGGATGCG CCGAGGGCCC CGCGTTCGCG CCGCGCAGAG	240
CCAGGCCCGC GGCCCGAGCC C ATG AGC ACC ATG CGC CTG CTG ACG CTC GCC	291
Met Ser Thr Met Arg Leu Leu Thr Leu Ala	10
CTG CTG TTC TCC TGC TCC GTC GCC CGT GCC GCG TGC GAC CCC AAG ATC	339
Leu Leu Phe Ser Cys Ser Val Ala Arg Ala Ala Cys Asp Pro Lys Ile	25
GTC AAC ATT GGC GCG GTG CTG AGC ACG CGG AAG CAC GAG CAG ATG TTC	387
Val Asn Ile Gly Ala Val Leu Ser Thr Arg Lys His Glu Gln Met Phe	40
CGC GAG GCC GTG AAC CAG GCC AAC AAG CGG CAC GGC TCC TGG AAG ATT	435
Arg Glu Ala Val Asn Gln Ala Asn Lys Arg His Gly Ser Trp Lys Ile	55
CAG CTC AAT GCC ACC TCC GTC ACG CAC AAG CCC AAC GCC ATC CAG ATG	483
Gln Leu Asn Ala Thr Ser Val Thr His Lys Pro Asn Ala Ile Gln Met	70
GCT CTG TCG GTG TGC GAG GAC CTC ATC TCC AGC CAG GTC TAC GCC ATC	531
Ala Leu Ser Val Cys Glu Asp Leu Ile Ser Ser Gln Val Tyr Ala Ile	90
CTA GTT AGC CAT CCA CCT ACC CCC AAC GAC CAC TTC ACT CCC ACC CCT	579
Leu Val Ser His Pro Pro Thr Pro Asn Asp His Phe Thr Pro Thr Pro	105
GTC TCC TAC ACA GCC GGC TTC TAC CGC ATA CCC GTG CTG GGG CTG ACC	627
Val Ser Tyr Thr Ala Gly Phe Tyr Arg Ile Pro Val Leu Gly Leu Thr	120
ACC CGC ATG TCC ATC TAC TCG GAC AAG AGC ATC CAC CTG AGC TTC CTG	675
Thr Arg Met Ser Ile Tyr Ser Asp Lys Ser Ile His Leu Ser Phe Leu	135
CGC ACC GTG CCG CCC TAC TCC CAC CAG TCC AGC GTG TGG TTT GAG ATG	723
Arg Thr Val Pro Pro Tyr Ser His Gln Ser Ser Val Trp Phe Glu Met	150
ATG CGT GTC TAC AGC TGG AAC CAC ATC ATC CTG CTG GTC AGC GAC GAC	771
Met Arg Val Tyr Ser Trp Asn His Ile Ile Leu Leu Val Ser Asp Asp	170
CAC GAG GGC CGG GCG GCT CAG AAA CGC CTG GAG ACG CTG CTG GAG GAG	819
His Glu Gly Arg Ala Ala Gln Lys Arg Leu Glu Thr Leu Leu Glu Glu	185
CGT GAG TCC AAG GCA GAG AAG GTG CTG CAG TTT GAC CCA GGG ACC AAG	867
Arg Glu Ser Lys Ala Glu Lys Val Leu Gln Phe Asp Pro Gly Thr Lys	200
AAC GTG ACG GCC CTG CTG ATG GAG GCG AAA GAG CTG GAG GCC CGG GTC	915
Asn Val Thr Ala Leu Leu Met Glu Ala Lys Glu Leu Glu Ala Arg Val	215

ATC Ile 220	ATC Ile 220	CTT Leu	TCT Ser	GCC Ala	AGC Ser	GAG Glu 225	GAC Asp	GAT Asp	GCT Ala	GCC Ala 230	ACT Thr	GTA Val	TAC Tyr	CGC Arg	GCA Ala	963
GCC Ala 235	GCG Ala	ATG Met	CTG Leu	AAC Asn	ATG Met 240	ACG Thr	GGC Gly	TCC Ser	GGG Gly 245	TAC Tyr 245	GTG Val	TGG Trp	CTG Leu	GTC Val	GGC Gly 250	1011
GAG Glu	CGC Arg	GAG Glu	ATC Ile	TCG Ser 255	GGG Gly	AAC Asn	GCC Ala	CTG Leu	CGC Arg 260	TAC Tyr	GCC Ala	CCA Pro	GAC Asp	GGC Gly 265	ATC Ile	1059
CTC Leu	GGG Gly	CTG Leu	CAG Gln 270	CTC Leu	ATC Ile	AAC Asn	GGC Gly	AAG Lys 275	AAC Asn	GAG Glu	TCG Ser	GCC Ala	CAC His 280	ATC Ile	AGC Ser	1107
GAC Asp	GCC Ala	GTG Val 285	GGC Gly	GTG Val	GTG Val	GCC Ala	CAG Gln 290	GCC Ala	GTG Val	CAC His	GAG Glu	CTC Leu 295	CTC Leu	GAG Glu	AAG Lys	1155
GAG Glu 300	AAC Asn	ATC Ile	ACC Thr	GAC Asp	CCG Pro	CCG Pro	CGG Arg 305	GGC Gly	TGC Cys	GTG Val	GGC Gly 310	AAC Asn	ACC Thr	AAC Asn	ATC Ile	1203
TGG Trp 315	AAG Lys	ACC Thr	GGG Gly	CCG Pro	CTC Leu 320	TTC Phe	AAG Lys	AGA Arg	GTG Val	CTG Leu 325	ATG Met	TCT Ser	TCC Ser	AAG Lys	TAT Tyr 330	1251
GCG Ala	GAT Asp	GGG Gly	GTG Val	ACT Thr 335	GGT Gly	CGC Arg	GTG Val	GAG Glu	TTC Phe 340	AAT Asn	GAG Glu	GAT Asp	GGG Gly	GAC Asp 345	CGG Arg	1299
AAG Lys	TTC Phe	GCC Ala	AAC Asn 350	TAC Tyr	AGC Ser	ATC Ile	ATG Met	AAC Asn 355	CTG Leu	CAG Gln	AAC Asn	CGC Arg	AAG Lys 360	CTG Leu	GTG Val	1347
CAA Gln	GTG Val	GGC Gly	ATC Ile 365	TAC Tyr	AAT Asn	GGC Gly	ACC Thr 370	CAC His	GTG Val	ATC Ile	CCT Pro	AAT Asn 375	GAC Asp	AGG Arg	AAG Lys	1395
ATC Ile 380	ATC Ile	TGG Trp	CCA Pro	GGC Gly	GGA Gly	GAG Glu 385	ACA Thr	GAG Glu	AAG Lys	CCT Pro	CGA Arg 390	GGG Gly	TAC Tyr	CAG Gln	ATG Met	1443
TCC Ser 395	ACC Thr	AGA Arg	CTG Leu	AAG Lys	ATT Ile 400	GTG Val	ACG Thr	ATC Ile	CAC His	CAG Gln 405	GAG Glu	CCC Pro	TTC Phe	GTG Val	TAC Tyr 410	1491
GTC Val	AAG Lys	CCC Pro	ACG Thr	CTG Leu 415	AGT Ser	GAT Asp	GGG Gly	ACA Thr	TGC Cys 420	AAG Lys	GAG Glu	GAG Glu	TTC Phe	ACA Thr 425	GTC Val	1539
AAC Asn	GGC Gly	GAC Asp	CCA Pro 430	GTC Val	AAG Lys	AAG Lys	GTG Val 435	ATC Ile	TGC Cys	ACC Thr	GGG Gly	CCC Pro	AAC Asn 440	GAC Asp	ACG Thr	1587
TCG Ser	CCG Pro	GGC Gly	AGC Ser 445	CCC Pro	CGC Arg	CAC His	ACG Thr 450	GTG Val	CCT Pro	CAG Gln	TGT Cys	TGC Cys 455	TAC Tyr	GGC Gly	TTT Phe	1635
TGC Cys 460	ATC Ile	GAC Asp	CTG Leu	CTC Leu	ATC Ile	AAG Lys 465	CTG Leu	GCA Ala	CGG Arg	ACC Thr	ATG Met 470	AAC Asn	TTC Phe	ACC Thr	TAC Tyr	1683
GAG Glu 475	GTG Val	CAC His	CTG Leu	GTG Val	GCA Ala 480	GAT Asp	GGC Gly	AAG Lys	TTC Phe	GGC Gly 485	ACA Thr	CAG Gln	GAG Glu	CGG Arg	GTG Val 490	1731

AAC	AAC	AGC	AAC	AAG	AAG	GAG	TGG	AAT	GGG	ATG	ATG	GGC	GAG	CTG	CTC	1779
Asn	Asn	Ser	Asn	Lys	Lys	Glu	Trp	Asn	Gly	Met	Met	Gly	Glu	Leu	Leu	
				495					500					505		
AGC	GGG	CAG	GCA	GAC	ATG	ATC	GTG	CGG	CCG	CTA	ACC	ATA	AAC	AAC	GAG	1827
Ser	Gly	Gln	Ala	Asp	Met	Ile	Val	Ala	Pro	Leu	Thr	Ile	Asn	Asn	Glu	
			510					515					520			
CGC	GCG	CAG	TAC	ATC	GAG	TTT	TCC	AAG	CCC	TTC	AAG	TAC	CAG	GGC	CTG	1875
Arg	Ala	Gln	Tyr	Ile	Glu	Phe	Ser	Lys	Pro	Phe	Lys	Tyr	Gln	Gly	Leu	
		525					530					535				
ACT	ATT	CTG	GTC	AAG	AAG	GAG	ATT	CCC	CGG	AGC	ACG	CTG	GAC	TCG	TTC	1923
Thr	Ile	Leu	Val	Lys	Lys	Glu	Ile	Pro	Arg	Ser	Thr	Leu	Asp	Ser	Phe	
	540					545					550					
ATG	CAG	CCG	TTC	CAG	AGC	ACA	CTG	TGG	CTG	CTG	GTG	GGG	CTG	TCG	GTG	1971
Met	Gln	Pro	Phe	Gln	Ser	Thr	Leu	Trp	Leu	Leu	Val	Gly	Leu	Ser	Val	
555					560					565					570	
CAC	GTG	GTG	GCC	GTG	ATG	CTG	TAC	CTG	CTG	GAC	CGC	TTC	AGC	CCC	TTC	2019
His	Val	Val	Ala	Val	Met	Leu	Tyr	Leu	Leu	Asp	Arg	Phe	Ser	Pro	Phe	
				575					580					585		
GGC	CGG	TTC	AAG	GTG	AAC	AGC	GAG	GAG	GAG	GAG	GAG	GAC	GCA	CTG	ACC	2067
Gly	Arg	Phe	Lys	Val	Asn	Ser	Glu	Glu	Glu	Glu	Glu	Asp	Ala	Leu	Thr	
			590					595					600			
CTG	TCC	TCG	GCC	ATG	TGG	TTC	TCC	TGG	GGC	GTG	CTG	CTC	AAC	TCC	GGC	2115
Leu	Ser	Ser	Ala	Met	Trp	Phe	Ser	Trp	Gly	Val	Leu	Leu	Asn	Ser	Gly	
		605					610					615				
ATC	GGG	GAA	GGC	GCC	CCC	AGA	AGC	TTC	TCA	GCG	CGC	ATC	CTG	GGC	ATG	2163
Ile	Gly	Glu	Gly	Ala	Pro	Arg	Ser	Phe	Ser	Ala	Arg	Ile	Leu	Gly	Met	
	620					625					630					
GTG	TGG	GCC	GGC	TTT	GCC	ATG	ATC	ATC	GTG	GCC	TCC	TAC	ACC	GCC	AAC	2211
Val	Trp	Ala	Gly	Phe	Ala	Met	Ile	Ile	Val	Ala	Ser	Tyr	Thr	Ala	Asn	
635					640				645						650	
CTG	GCG	GCC	TTC	CTG	GTG	CTG	GAC	CGG	CCG	GAG	GAG	CGC	ATC	ACG	GGC	2259
Leu	Ala	Ala	Phe	Leu	Val	Leu	Asp	Arg	Pro	Glu	Glu	Arg	Ile	Thr	Gly	
				655					660				665			
ATC	AAC	GAC	CCT	CGG	CTG	AGG	AAC	CCC	TCG	GAC	AAG	TTT	ATC	TAC	GCC	2307
Ile	Asn	Asp	Pro	Arg	Leu	Arg	Asn	Pro	Ser	Asp	Lys	Phe	Ile	Tyr	Ala	
			670					675					680			
ACG	GTG	AAG	CAG	AGC	TCC	GTG	GAT	ATC	TAC	TTC	CGG	CGC	CAG	GTG	GAG	2355
Thr	Val	Lys	Gln	Ser	Ser	Val	Asp	Ile	Tyr	Phe	Arg	Arg	Gln	Val	Glu	
		685					690					695				
CTG	AGC	ACC	ATG	TAC	CGG	CAT	ATG	GAG	AAG	CAC	AAC	TAC	GAG	AGT	GCG	2403
Leu	Ser	Thr	Met	Tyr	Arg	His	Met	Glu	Lys	His	Asn	Tyr	Glu	Ser	Ala	
		700				705					710					
GCG	GAG	GCC	ATC	CAG	GCC	GTG	AGA	GAC	AAC	AAG	CTG	CAT	GCC	TTC	ATC	2451
Ala	Glu	Ala	Ile	Gln	Ala	Val	Arg	Asp	Asn	Lys	Leu	His	Ala	Phe	Ile	
715					720					725					730	
TGG	GAC	TCG	GCG	GTG	CTG	GAG	TTC	GAG	GCC	TCG	CAG	AAG	TGC	GAC	CTG	2499
Trp	Asp	Ser	Ala	Val	Leu	Glu	Phe	Glu	Ala	Ser	Gln	Lys	Cys	Asp	Leu	
				735					740				745			
GTG	ACG	ACT	GGA	GAG	CTG	TTT	TTC	CGC	TCG	GGC	TTC	GGC	ATA	GGC	ATG	2547
Val	Thr	Thr	Gly	Glu	Leu	Phe	Phe	Arg	Ser	Gly	Phe	Gly	Ile	Gly	Met	
			750					755					760			

CGC AAA GAC AGC CCC TGG AAG CAG AAC GTC TCC CTG TCC ATC CTC AAG	2595
Arg Lys Asp Ser Pro Trp Lys Gln Asn Val Ser Leu Ser Ile Leu Lys	
765 770 775	
TCC CAC GAG AAT GGC TTC ATG GAA GAC CTG GAC AAG ACG TGG GTT CGG	2643
Ser His Glu Asn Gly Phe Met Glu Asp Leu Asp Lys Thr Trp Val Arg	
780 785 790	
TAT CAG GAA TGT GAC TCG CGC AGC AAC GCC CCT GCG ACC CTT ACT TTT	2691
Tyr Gln Glu Cys Asp Ser Arg Ser Asn Ala Pro Ala Thr Leu Thr Phe	
795 800 805 810	
GAG AAC ATG GCC GGG GTC TTC ATG CTG GTA GCT GGG GGC ATC GTG GCC	2739
Glu Asn Met Ala Gly Val Phe Met Leu Val Ala Gly Gly Ile Val Ala	
815 820 825	
GGG ATC TTC CTG ATT TTC ATC GAG ATT GCC TAC AAG CGG CAC AAG GAT	2787
Gly Ile Phe Leu Ile Phe Ile Glu Ile Ala Tyr Lys Arg His Lys Asp	
830 835 840	
GCT CGC CGG AAG CAG ATG CAG CTG GCC TTT GCC GCC GTT AAC GTG TGG	2835
Ala Arg Arg Lys Gln Met Gln Leu Ala Phe Ala Ala Val Asn Val Trp	
845 850 855	
CGG AAG AAC CTG CAG GAT AGA AAG AGT GGT AGA GCA GAG CCT GAC CCT	2883
Arg Lys Asn Leu Gln Asp Arg Lys Ser Gly Arg Ala Glu Pro Asp Pro	
860 865 870	
AAA AAG AAA GCC ACA TTT AGG GCT ATC ACC TCC ACC CTG GCT TCC AGC	2931
Lys Lys Lys Ala Thr Phe Arg Ala Ile Thr Ser Thr Leu Ala Ser Ser	
875 880 885 890	
TTC AAG AGG CGT AGG TCC TCC AAA GAC ACG AGC ACC GGG GGT GGA CGC	2979
Phe Lys Arg Arg Arg Ser Ser Lys Asp Thr Ser Thr Gly Gly Gly Arg	
895 900 905	
GGT GCT TTG CAA AAC CAA AAA GAC ACA GTG CTG CCG CGA CGC GCT ATT	3027
Gly Ala Leu Gln Asn Gln Lys Asp Thr Val Leu Pro Arg Arg Ala Ile	
910 915 920	
GAG AGG GAG GAG GGC CAG CTG CAG CTG TGT TCC CGT CAT AGG GAG AGC	3075
Glu Arg Glu Glu Gly Gln Leu Gln Leu Cys Ser Arg His Arg Glu Ser	
925 930 935	
TGAGACTCCC CGCCCCGCCCT CCTCTGCCCC CTCCCCCGCA GACAGACAGA CAGACGGACG	3135
GGACAGCGGC CCGGCCCCACG CAGAGCCCCG GAGCACCACG GGGTCGGGGG AGGAGCACCC	3195
CCAGCCTCCC CCAGGCTGCG CCTGCCCGCC CGCCGGTTGG CCGGCTGGCC GGTCCACCCC	3255
GTCCCGGCCC CGCGCGTGCC CCCAGCGTGG GGCTAACGGG CGCCTTGCT GTGTATTTCT	3315
ATTTTGCAGC AGTACCATCC CACTGATATC ACGGGCCCCG TCAACCTCTC AGATCCCTCG	3375
GTCAGCACCG TGGTGTGAGG CCCCCGGAGG CGCCACCTG CCCAGTTAGC CCGGCCAAGG	3435
ACACTGATGG GTCCTGCTGC TCGGGAAGGC CTGAGGGAAG CCCACCCGCC CCAGAGACTG	3495
CCCACCCTGG GCCTCCCGTC CGTCCGCCCG CCCACCCCGC TGCCTGGCGG GCAGCCCCTG	3555
CTGGACCAAG GTGCGGACCG GAGCGGCTGA GGACGGGGCA GAGCTGAGTC GGCTGGGCAG	3615
GGCCGCAGGG CGCTCCGGCA GAGGCAGGCC CCTGGGGTCT CTGAGCAGTG GGGAGCGGGG	3675
GCTAACTGCC CCCAGGCGGA GGGGCTTGGA GCAGAGACGG CAGCCCCATC CTTCCCGCAG	3735
CACCAGCCTG AGCCACAGTG GGGCCCATGG CCCCAGCTGG CTGGGTGCGC CCTCCTCGGG	3795

CGCCTGCGCT CCTCTGCAGC CTGAGCTCCA CCCTCCCCTC TTCTTGCGGC ACCGCCCACC 3855
 AAACACCCCG TCTGCCCCCTT GACGCCACAC GCCGGGGCTG GCGCTGCCCT CCCCCACGGC 3915
 CGTCCCTGAC TTCCCAGCTG GCAGCGCCTC CCGCCGCCTC GGGCCGCCTC CTCCAGAATC 3975
 GAGAGGGCTG AGCCCCCTCT CTCCTCGTCC GGCCTGCAGC ACAGAAGGGG GCCTCCCCGG 4035
 GGGTCCCCGG ACGCTGGCTC GGGACTGTCT TCAACCCTGC CCTGCACCTT GGGCACGGGA 4095
 GAGCGCCACC CGCCCGCCCC CGCCCTCGCT CCGGGTGCCT GACCGGCCCC CCACCTTGTA 4155
 CAGAACCAGC ACTCCCAGGG CCGAGCGCG TGCCTTCCCC GTGCGCAGCC GCGCTCTGCC 4215
 CCTCCGTCCC CAGGGTGCAG GCGCGCACCG CCCAACCCCC ACCTCCCGGT GTATGCAGTG 4275
 GTGATGCCTA AAGGAATGTC ACG 4298

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 938 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Ser Thr Met Arg Leu Leu Thr Leu Ala Leu Leu Phe Ser Cys Ser
 1 5 10 15
 Val Ala Arg Ala Ala Cys Asp Pro Lys Ile Val Asn Ile Gly Ala Val
 20 25 30
 Leu Ser Thr Arg Lys His Glu Gln Met Phe Arg Glu Ala Val Asn Gln
 35 40 45
 Ala Asn Lys Arg His Gly Ser Trp Lys Ile Gln Leu Asn Ala Thr Ser
 50 55 60
 Val Thr His Lys Pro Asn Ala Ile Gln Met Ala Leu Ser Val Cys Glu
 65 70 75 80
 Asp Leu Ile Ser Ser Gln Val Tyr Ala Ile Leu Val Ser His Pro Pro
 85 90 95
 Thr Pro Asn Asp His Phe Thr Pro Thr Pro Val Ser Tyr Thr Ala Gly
 100 105 110
 Phe Tyr Arg Ile Pro Val Leu Gly Leu Thr Thr Arg Met Ser Ile Tyr
 115 120 125
 Ser Asp Lys Ser Ile His Leu Ser Phe Leu Arg Thr Val Pro Pro Tyr
 130 135 140
 Ser His Gln Ser Ser Val Trp Phe Glu Met Met Arg Val Tyr Ser Trp
 145 150 155 160
 Asn His Ile Ile Leu Leu Val Ser Asp Asp His Glu Gly Arg Ala Ala
 165 170 175
 Gln Lys Arg Leu Glu Thr Leu Leu Glu Glu Arg Glu Ser Lys Ala Glu
 180 185 190

Lys Val Leu Gln Phe Asp Pro Gly Thr Lys Asn Val Thr Ala Leu Leu
 195 200 205
 Met Glu Ala Lys Glu Leu Glu Ala Arg Val Ile Ile Leu Ser Ala Ser
 210 215 220
 Glu Asp Asp Ala Ala Thr Val Tyr Arg Ala Ala Ala Met Leu Asn Met
 225 230 235 240
 GlyThr Gly Ser Gly Tyr Val Trp Leu Val Gly Glu Arg Glu Ile Ser
 245 250 255
 Asn Ala Leu Arg Tyr Ala Pro Asp Gly Ile Leu Gly Leu Gln Leu Ile
 260 265 270
 Asn Gly Lys Asn Glu Ser Ala His Ile Ser Asp Ala Val Gly Val Val
 275 280 285
 Ala Gln Ala Val His Glu Leu Leu Glu Lys Glu Asn Ile Thr Asp Pro
 290 295 300
 Pro Arg Gly Cys Val Gly Asn Thr Asn Ile Trp Lys Thr Gly Pro Leu
 305 310 315 320
 Phe Lys Arg Val Leu Met Ser Ser Lys Tyr Ala Asp Gly Val Thr Gly
 325 330 335
 Arg Val Glu Phe Asn Glu Asp Gly Asp Arg Lys Phe Ala Asn Tyr Ser
 340 345 350
 Ile Met Asn Leu Gln Asn Arg Lys Leu Val Gln Val Gly Ile Tyr Asn
 355 360 365
 Gly Thr His Val Ile Pro Asn Asp Arg Lys Ile Ile Trp Pro Gly Gly
 370 375 380
 Glu Thr Glu Lys Pro Arg Gly Tyr Gln Met Ser Thr Arg Leu Lys Ile
 385 390 395 400
 Val Thr Ile His Gln Glu Pro Phe Val Tyr Val Lys Pro Thr Leu Ser
 405 410 415
 Asp Gly Thr Cys Lys Glu Glu Phe Thr Val Asn Gly Asp Pro Val Lys
 420 425 430
 Lys Val Ile Cys Thr Gly Pro Asn Asp Thr Ser Pro Gly Ser Pro Arg
 435 440 445
 His Thr Val Pro Gln Cys Cys Tyr Gly Phe Cys Ile Asp Leu Leu Ile
 450 455 460
 Lys Leu Ala Arg Thr Met Asn Phe Thr Tyr Glu Val His Leu Val Ala
 465 470 475 480
 Asp Gly Lys Phe Gly Thr Gln Glu Arg Val Asn Asn Ser Asn Lys Lys
 485 490 495
 Glu Trp Asn Gly Met Met Gly Glu Leu Leu Ser Gly Gln Ala Asp Met
 500 505 510
 Ile Val Ala Pro Leu Thr Ile Asn Asn Glu Arg Ala Gln Tyr Ile Glu
 515 520 525
 Phe Ser Lys Pro Phe Lys Tyr Gln Gly Leu Thr Ile Leu Val Lys Lys
 530 535 540

Glu Ile Pro Arg Ser Thr Leu Asp Ser Phe Met Gln Pro Phe Gln Ser
 545 550 555 560
 Thr Leu Trp Leu Leu Val Gly Leu Ser Val His Val Val Ala Val Met
 565 570 575
 Leu Tyr Leu Leu Asp Arg Phe Ser Pro Phe Gly Arg Phe Lys Val Asn
 580 585 590
 Ser Glu Glu Glu Glu Glu Asp Ala Leu Thr Leu Ser Ser Ala Met Trp
 595 600 605
 Phe Ser Trp Gly Val Leu Leu Asn Ser Gly Ile Gly Glu Gly Ala Pro
 610 615 620
 Arg Ser Phe Ser Ala Arg Ile Leu Gly Met Val Trp Ala Gly Phe Ala
 625 630 635 640
 Met Ile Ile Val Ala Ser Tyr Thr Ala Asn Leu Ala Ala Phe Leu Val
 645 650 655
 Leu Asp Arg Pro Glu Glu Arg Ile Thr Gly Ile Asn Asp Pro Arg Leu
 660 665 670
 Arg Asn Pro Ser Asp Lys Phe Ile Tyr Ala Thr Val Lys Gln Ser Ser
 675 680 685
 Val Asp Ile Tyr Phe Arg Arg Gln Val Glu Leu Ser Thr Met Tyr Arg
 690 695 700
 His Met Glu Lys His Asn Tyr Glu Ser Ala Ala Glu Ala Ile Gln Ala
 705 710 715 720
 Val Arg Asp Asn Lys Leu His Ala Phe Ile Trp Asp Ser Ala Val Leu
 725 730 735
 Glu Phe Glu Ala Ser Gln Lys Cys Asp Leu Val Thr Thr Gly Glu Leu
 740 745 750
 Phe Phe Arg Ser Gly Phe Gly Ile Gly Met Arg Lys Asp Ser Pro Trp
 755 760 765
 Lys Gln Asn Val Ser Leu Ser Ile Leu Lys Ser His Glu Asn Gly Phe
 770 775 780
 Met Glu Asp Leu Asp Lys Thr Trp Val Arg Tyr Gln Glu Cys Asp Ser
 785 790 795 800
 Arg Ser Asn Ala Pro Ala Thr Leu Thr Phe Glu Asn Met Ala Gly Val
 805 810 815
 Phe Met Leu Val Ala Gly Gly Ile Val Ala Gly Ile Phe Leu Ile Phe
 820 825 830
 Ile Glu Ile Ala Tyr Lys Arg His Lys Asp Ala Arg Arg Lys Gln Met
 835 840 845
 Gln Leu Ala Phe Ala Ala Val Asn Val Trp Arg Lys Asn Leu Gln Asp
 850 855 860
 Arg Lys Ser Gly Arg Ala Glu Pro Asp Pro Lys Lys Lys Ala Thr Phe
 865 870 875 880
 Arg Ala Ile Thr Ser Thr Leu Ala Ser Ser Phe Lys Arg Arg Arg Ser
 885 890 895

Ser Lys Asp Thr Ser Thr Gly Gly Gly Arg Gly Ala Leu Gln Asn Gln
 900 905 910

Lys Asp Thr Val Leu Pro Arg Arg Ala Ile Glu Arg Glu Glu Gly Gln
 915 920 925

Leu Gln Leu Cys Ser Arg His Arg Glu Ser
 930 935

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 63 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 1..63

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

AGT AAA AAA AGG AAC TAT GAA AAC CTC GAC CAA CTG TCC TAT GAC AAC	48
Ser Lys Lys Arg Asn Tyr Glu Asn Leu Asp Gln Leu Ser Tyr Asp Asn	
1 5 10 15	
AAG CGC GGA CCC AAG	63
Lys Arg Gly Pro Lys	
20	

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Ser Lys Lys Arg Asn Tyr Glu Asn Leu Asp Gln Leu Ser Tyr Asp Asn
1 5 10 15
Lys Arg Gly Pro Lys
20

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 4340 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 189..3899

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CCCTTAATAA GATTTGCCAC GTACACTCGA GCCATCGCGA GTGTCCTTGA GCCGCGGGTG	60
ACGGTGGCTC TCGCTGCTCG CGCCCCCTCC TCCCGCGGGG GGAGCCTGAT GCCACGTTCC	120
CTATGAATTA TTTATCGCCG GCCTAAAAAT ACCCCGAACT TCACAGCCCC AGTGACCCTC	180
CGGTGGAC ATG GGT GGG GCC CTG GGG CCG GCC CTG TTG CTC ACC TCG CTC	230
Met Gly Gly Ala Leu Gly Pro Ala Leu Leu Leu Thr Ser Leu	
1 5 10	
TTC GGT GCC TGG GCA GGG CTG GGT CCG GGG CAG GGC GAG CAG GGC ATG	278
Phe Gly Ala Trp Ala Gly Leu Gly Pro Gly Gln Gly Glu Gln Gly Met	
15 20 25 30	
ACG GTG GCC GTG GTG TTT AGC AGC TCA GGG CCG CCC CAG GCC CAG TTC	326
Thr Val Ala Val Val Phe Ser Ser Ser Gly Pro Pro Gln Ala Gln Phe	
35 40 45	
CGT GTC CGC CTC ACC CCC CAG AGC TTC CTG GAC CTA CCC CTG GAG ATC	374
Arg Val Arg Leu Thr Pro Gln Ser Phe Leu Asp Leu Pro Leu Glu Ile	
50 55 60	
CAG CCG CTC ACA GTT GGG GTC AAC ACC ACC AAC CCC AGC AGC CTC CTC	422
Gln Pro Leu Thr Val Gly Val Asn Thr Thr Asn Pro Ser Ser Leu Leu	
65 70 75	
ACC CAG ATC TGC GGC CTC CTG GGT GCT GCC CAC GTC CAC GGC ATT GTC	470
Thr Gln Ile Cys Gly Leu Leu Gly Ala Ala His Val His Gly Ile Val	
80 85 90	
TTT GAG GAC AAC GTG GAC ACC GAG GCG GTG GCC CAG ATC CTT GAC TTC	518
Phe Glu Asp Asn Val Asp Thr Glu Ala Val Ala Gln Ile Leu Asp Phe	
95 100 105 110	
ATC TCC TCC CAG ACC CAT GTG CCC ATC CTC AGC ATC AGC GGA GGC TCT	566
Ile Ser Ser Gln Thr His Val Pro Ile Leu Ser Ile Ser Gly Gly Ser	
115 120 125	
GCT GTG GTC CTC ACC CCC AAG GAG CCG GGC TCC GCC TTC CTG CAG CTG	614
Ala Val Val Leu Thr Pro Lys Glu Pro Gly Ser Ala Phe Leu Gln Leu	
130 135 140	
GGC GTG TCC CTG GAG CAG CAG CTG CAG GTG CTG TTC AAG GTG CTG GAA	662
Gly Val Ser Leu Glu Gln Gln Leu Gln Val Leu Phe Lys Val Leu Glu	
145 150 155	
GAG TAC GAC TGG AGC GCC TTC GCC GTC ATC ACC AGC CTG CAC CCG GGC	710
Glu Tyr Asp Trp Ser Ala Phe Ala Val Ile Thr Ser Leu His Pro Gly	
160 165 170	
CAC GCG CTC TTC CTG GAG GGC GTG CCG GCC GTC GCC GAC GCC AGC CAC	758
His Ala Leu Phe Leu Glu Gly Val Arg Ala Val Ala Asp Ala Ser His	
175 180 185 190	
GTG AGT TGG CCG CTG CTG GAC GTG GTC ACG CTG GAA CTG GAC CCG GGA	806
Val Ser Trp Arg Leu Leu Asp Val Val Thr Leu Glu Leu Asp Pro Gly	
195 200 205	

GGG CCG CGC GCG CGC ACG CAG CGC CTG CTG CGC CAG CTC GAC GCG CCC Gly Pro Arg Ala Arg Thr Gln Arg Leu Leu Arg Gln Leu Asp Ala Pro 210 215 220	854
GTG TTT GTG GCC TAC TGC TCG CGC GAG GAG GCC GAG GTG CTC TTC GCC Val Phe Val Ala Tyr Cys Ser Arg Glu Glu Ala Glu Val Leu Phe Ala 225 230 235	902
GAG GCG GCG CAG GCC GGT CTG GTG GGG CCC GGC CAC GTG TGG CTG GTG Glu Ala Ala Gln Ala Gly Leu Val Gly Pro Gly His Val Trp Leu Val 240 245 250	950
CCC AAC CTG GCG CTG GGC AGC ACC GAT GCG CCC CCC GCC ACC TTC CCC Pro Asn Leu Ala Leu Gly Ser Thr Asp Ala Pro Ala Thr Phe Pro 255 260 265 270	998
GTG GGC CTC ATC AGC GTC GTC ACC GAG AGC TGG CGC CTC AGC CTG CGC Val Gly Leu Ile Ser Val Val Thr Glu Ser Trp Arg Leu Ser Leu Arg 275 280 285	1046
CAG AAG GTG CGC GAC GGC GTG GCC ATT CTG GCC CTG GGC GCC CAC AGC Gln Lys Val Arg Asp Gly Val Ala Ile Leu Ala Leu Gly Ala His Ser 290 295 300	1094
TAC TGG CGC CAG CAT GGA ACC CTG CCA GCC CCG GCC GGG GAC TGC CGT Tyr Trp Arg Gln His Gly Thr Leu Pro Ala Pro Ala Gly Asp Cys Arg 305 310 315	1142
GTT CAC CCT GGG CCC GTC AGC CCT GCC CGG GAG GCC TTC TAC AGG CAC Val His Pro Gly Pro Val Ser Pro Ala Arg Glu Ala Phe Tyr Arg His 320 325 330	1190
CTA CTG AAT GTC ACC TGG GAG GGC CGA GAC TTC TCC TTC AGC CCT GGT Leu Leu Asn Val Thr Trp Glu Gly Arg Asp Phe Ser Phe Ser Pro Gly 335 340 345 350	1238
GGG TAC CTG GTC CAG CCC ACC ATG GTG GTG ATC GCC CTC AAC CGG CAC Gly Tyr Leu Val Gln Pro Thr Met Val Val Ile Ala Leu Asn Arg His 355 360 365	1286
CGC CTC TGG GAG ATG GTG GGG CGC TGG GAG CAT GGC GTC CTA TAC ATG Arg Leu Trp Glu Met Val Gly Arg Trp Glu His Gly Val Leu Tyr Met 370 375 380	1334
AAG TAC CCC GTG TGG CCT CGC TAC AGT GCC TCT CTG CAG CCT GTG GTG Lys Tyr Pro Val Trp Pro Arg Tyr Ser Ala Ser Leu Gln Pro Val Val 385 390 395	1382
GAC AGT CGG CAC CTG ACG GTG GCC ACG CTG GAA GAG CGG CCC TTT GTC Asp Ser Arg His Leu Thr Val Ala Thr Leu Glu Glu Arg Pro Phe Val 400 405 410	1430
ATC GTG GAG AGC CCT GAC CCT GGC ACA GGA GGC TGT GTC CCC AAC ACC Ile Val Glu Ser Pro Asp Pro Gly Thr Gly Gly Cys Val Pro Asn Thr 415 420 425 430	1478
GTG CCC TGC CGC AGG CAG AGC AAC CAC ACC TTC AGC AGC GGG GAC GTG Val Pro Cys Arg Arg Gln Ser Asn His Thr Phe Ser Ser Gly Asp Val 435 440 445	1526
GCC CCC TAC ACC AAG CTC TGC TGT AAG GGA TTC TGC ATC GAC ATC CTC Ala Pro Tyr Thr Lys Leu Cys Cys Lys Gly Phe Cys Ile Asp Ile Leu 450 455 460	1574
AAG AAG CTG GCC AGA GTG GTC AAA TTC TCC TAC GAC CTG TAC CTG GTG Lys Lys Leu Ala Arg Val Val Lys Phe Ser Tyr Asp Leu Tyr Leu Val 465 470 475	1622

ACC	AAC	GGC	AAG	CAT	GGC	AAG	CGG	GTG	CGC	GGC	GTA	TGG	AAC	GGC	ATG	1670
Thr	Asn	Gly	Lys	His	Gly	Lys	Arg	Val	Arg	Gly	Val	Trp	Asn	Gly	Met	
	480					485					490					
ATT	GGG	GAG	GTG	TAC	TAC	AAG	CGG	GCA	GAC	ATG	GCC	ATC	GGC	TCC	CTC	1718
Ile	Gly	Glu	Val	Tyr	Tyr	Lys	Arg	Ala	Asp	Met	Ala	Ile	Gly	Ser	Leu	
495					500					505					510	
ACC	ATC	AAT	GAG	GAA	CGC	TCC	GAG	ATC	GTA	GAC	TTC	TCT	GTA	CCC	TTT	1766
Thr	Ile	Asn	Glu		Arg	Ser	Glu	Ile	Val	Asp	Phe	Ser	Val	Pro	Phe	
				515					520					525		
GTG	GAG	ACG	GGC	ATC	AGT	GTG	ATG	GTG	GCT	CGC	AGC	AAT	GGC	ACC	GTC	1814
Val	Glu	Thr	Gly	Ile	Ser	Val	Met	Val	Ala	Arg	Ser	Asn	Gly	Thr	Val	
			530					535					540			
TCC	CCC	TCG	GCC	TTC	TTG	GAG	CCA	TAT	AGC	CCT	GCA	GTG	TGG	GTG	ATG	1862
Ser	Pro	Ser	Ala	Phe	Leu	Glu	Pro	Tyr	Ser	Pro	Ala	Val	Trp	Val	Met	
		545					550					555				
ATG	TTT	GTC	ATG	TGC	CTC	ACT	GTG	GTG	GCC	ATC	ACC	GTC	TTC	ATG	TTC	1910
Met	Phe	Val	Met	Cys	Leu	Thr	Val	Val	Ala	Ile	Thr	Val	Phe	Met	Phe	
	560					565					570					
GAG	TAC	TTC	AGC	CCT	GTC	AGC	TAC	AAC	CAG	AAC	CTC	ACC	AGA	GGC	AAG	1958
Glu	Tyr	Phe	Ser	Pro	Val	Ser	Tyr	Asn	Gln	Asn	Leu	Thr	Arg	Gly	Lys	
575					580					585					590	
AAG	TCC	GGG	GGC	CCA	GCT	TTC	ACT	ATC	GGC	AAG	TCC	GTG	TGG	CTG	CTG	2006
Lys	Ser	Gly	Gly	Pro	Ala	Phe	Thr	Ile	Gly	Lys	Ser	Val	Trp	Leu	Leu	
				595					600					605		
TGG	GCG	CTG	GTC	TTC	AAC	AAC	TCA	GTG	CCC	ATC	GAG	AAC	CCG	CGG	GGC	2054
Trp	Ala	Leu	Val	Phe	Asn	Asn	Ser	Val	Pro	Ile	Glu	Asn	Pro	Arg	Gly	
			610					615					620			
ACC	ACC	AGC	AAG	ATC	ATG	GTT	CTG	GTC	TGG	GCC	TTC	TTT	GCT	GTC	ATC	2102
Thr	Thr	Ser	Lys	Ile	Met	Val	Leu	Val	Trp	Ala	Phe	Phe	Ala	Val	Ile	
		625					630					635				
TTC	CTC	GCC	AGA	TAC	ACG	GCC	AAC	CTG	GCC	GCC	TTC	ATG	ATC	CAA	GAG	2150
Phe	Leu	Ala	Arg	Tyr	Thr	Ala	Asn	Leu	Ala	Ala	Phe	Met	Ile	Gln	Glu	
	640					645					650					
CAA	TAC	ATC	GAC	ACT	GTG	TCG	GGC	CTC	AGT	GAC	AAG	AAG	TTT	CAG	CGG	2198
Gln	Tyr	Ile	Asp	Thr	Val	Ser	Gly	Leu	Ser	Asp	Lys	Lys	Phe	Gln	Arg	
655					660					665					670	
CCT	CAA	GAT	CAG	TAC	CCA	CCT	TTC	CGC	TTC	GGC	ACG	GTG	CCC	AAC	GGC	2246
Pro	Gln	Asp	Gln	Tyr	Pro	Pro	Phe	Arg	Phe	Gly	Thr	Val	Pro	Asn	Gly	
				675					680					685		
AGC	ACG	GAG	CGG	AAC	ATC	CGC	AGT	AAC	TAC	CGT	GAC	ATG	CAC	ACC	CAC	2294
Ser	Thr	Glu	Arg	Asn	Ile	Arg	Ser	Asn	Tyr	Arg	Asp	Met	His	Thr	His	
			690					695					700			
ATG	GTC	AAG	TTC	AAC	CAG	CGC	TCG	GTG	GAG	GAC	GCG	CTC	ACC	AGC	CTC	2342
Met	Val	Lys	Phe	Asn	Gln	Arg	Ser	Val	Glu	Asp	Ala	Leu	Thr	Ser	Leu	
		705					710					715				
AAG	ATG	GGG	AAG	CTG	GAT	GCC	TTC	ATC	TAT	GAT	GCT	GCT	GTC	CTC	AAC	2390
Lys	Met	Gly	Lys	Leu	Asp	Ala	Phe	Ile	Tyr	Asp	Ala	Ala	Val	Leu	Asn	
	720					725					730					
TAC	ATG	GCA	GGC	AAG	GAC	GAG	GGC	TGC	AAG	CTG	GTC	ACC	ATT	GGG	TCT	2438
Tyr	Met	Ala	Gly	Lys	Asp	Glu	Gly	Cys	Lys	Leu	Val	Thr	Ile	Gly	Ser	
735					740					745					750	

GGC AAG GTC TTT GCT ACC ACT GGC TAC GGC ATC GCC ATG CAG AAG GAC Gly Lys Val Phe Ala Thr Thr Gly Tyr Gly Ile Ala Met Gln Lys Asp 755 760 765	2486
TCC CAC TGG AAG CGG GCC ATA GAC CTG GCG CTC TTG CAG TTC CTG GCG Ser His Trp Lys Arg Ala Ile Asp Leu Ala Leu Leu Gln Phe Leu Gly 770 775 780	2534
GAC GGA GAG ACA CAG AAA CTG GAG ACA GTG TGG CTC TCA GGG ATC TGC Asp Gly Glu Thr Gln Lys Leu Glu Thr Val Trp Leu Ser Gly Ile Cys 785 790 795	2582
CAG AAT GAG AAG AAC GAG GTG ATG AGC AGC AAG CTG GAC ATC GAC AAC Gln Asn Glu Lys Asn Glu Val Met Ser Ser Lys Leu Asp Ile Asp Asn 800 805 810	2630
ATG GCA GGC GTC TTC TAC ATG CTG CTG GTG GCC ATG GGG CTG GCC CTG Met Ala Gly Val Phe Tyr Met Leu Leu Val Ala Met Gly Leu Ala Leu 815 820 825 830	2678
CTG GTC TTC GCC TGG GAG CAC CTG GTC TAC TGG AAG CTG CGC CAC TCG Leu Val Phe Ala Trp Glu His Leu Val Tyr Trp Lys Leu Arg His Ser 835 840 845	2726
GTG CCC AAC TCA TCC CAG CTG GAC TTC CTG CTG GCT TTC AGC AGG GGC Val Pro Asn Ser Ser Gln Leu Asp Phe Leu Leu Ala Phe Ser Arg Gly 850 855 860	2774
ATC TAC AGC TGC TTC AGC GGG GTG CAG AGC CTC GCC AGC CCA CCG CGG Ile Tyr Ser Cys Phe Ser Gly Val Gln Ser Leu Ala Ser Pro Pro Arg 865 870 875	2822
CAG GCC AGC CCG GAC CTC ACG GCC AGC TCG GCC CAG GCC AGC GTG CTC Gln Ala Ser Pro Asp Leu Thr Ala Ser Ser Ala Gln Ala Ser Val Leu 880 885 890	2870
AAG ATG CTG CAG GCA GCC CGC GAC ATG GTG ACC ACG GCG GGC GTA AGC Lys Met Leu Gln Ala Ala Arg Asp Met Val Thr Thr Ala Gly Val Ser 895 900 905 910	2918
AGC TCC CTG GAC CGC GCC ACT CGC ACC ATC GAG AAT TGG GGT GGC GGC Ser Ser Leu Asp Arg Ala Thr Arg Thr Ile Glu Asn Trp Gly Gly Gly 915 920 925	2966
CGC CGT GCG CCC CCA CCG TCC CCC TGC CCG ACC CCG CGG TCT GGC CCC Arg Arg Ala Pro Pro Pro Ser Pro Cys Pro Thr Pro Arg Ser Gly Pro 930 935 940	3014
AGC CCA TGC CTG CCC ACC CCC GAC CCG CCC CCA GAG CCG AGC CCC ACG Ser Pro Cys Leu Pro Thr Pro Asp Pro Pro Pro Glu Pro Ser Pro Thr 945 950 955	3062
GGC TGG GGA CCG CCA GAC GGG GGT CGC GCG GCG CTT GTG CGC AGG GCT Gly Trp Gly Pro Pro Asp Gly Gly Arg Ala Ala Leu Val Arg Arg Ala 960 965 970	3110
CCG CAG CCC CCG GGC CGC CCC CCG ACG CCG GGG CCG CCC CTG TCC GAC Pro Gln Pro Pro Gly Arg Pro Pro Thr Pro Gly Pro Pro Leu Ser Asp 975 980 985 990	3158
GTC TCC CGA GTG TCG CGC CGC CCA GCC TGG GAG GCG CGG TGG CCG GTG Val Ser Arg Val Ser Arg Arg Pro Ala Trp Glu Ala Arg Trp Pro Val 995 1000 1005	3206
CGG ACC GGG CAC TGC GGG AGG CAC CTC TCG GCC TCC GAG CGG CCC CTG Arg Thr Gly His Cys Gly Arg His Leu Ser Ala Ser Glu Arg Pro Leu 1010 1015 1020	3254

TCG CCC GCG CGC TGT CAC TAC AGC TCC TTT CCT CGA GCC GAC CGA TCC Ser Pro Ala Arg Cys His Tyr Ser Ser Phe Pro Arg Ala Asp Arg Ser 1025 1030 1035	3302
GGC CGC CCC TTC CTC CCG CTC TTC CCG GAG CCC CCG GAG CTG GAG GAC Gly Arg Pro Phe Leu Pro Leu Phe Pro Glu Pro Pro Glu Leu Glu Asp 1040 1045 1050	3350
CTG CCG CTG CTC TGT CCG GAG CAG CTG GCC CCG CCG GAG GCC CTG CTG Leu Pro Leu Leu Gly Pro Glu Gln Leu Ala Arg Arg Glu Ala Leu Leu 1055 1060 1065 1070	3398
CAC GCG GCC TGG GCC CGG GGC TCG CGC CCG CGT CAC GCT TCC CTG CCC His Ala Ala Trp Ala Arg Gly Ser Arg Pro Arg His Ala Ser Leu Pro 1075 1080 1085	3446
AGC TCC GTG GCC GAG GCC TTC GCT CGG CCC AGC TCG CTG CCC GCT GGG Ser Ser Val Ala Glu Ala Phe Ala Arg Pro Ser Ser Leu Pro Ala Gly 1090 1095 1100	3494
TGC ACC GGC CCC GCC TGC GCC CGC CCC GAC GGA CAC TCG GCC TGC AGG Cys Thr Gly Pro Ala Cys Ala Arg Pro Asp Gly His Ser Ala Cys Arg 1105 1110 1115	3542
CGC TTG GCG CAG GCG CAG TCG ATG TGC TTG CCG ATC TAC CGG GAG GCC Arg Leu Ala Gln Ala Gln Ser Met Cys Leu Pro Ile Tyr Arg Glu Ala 1120 1125 1130	3590
TGC CAG GAG GGC GAG CAG GCA GGG GCC CCC GCC TGG CAG CAC AGA CAG Cys Gln Glu Gly Glu Gln Ala Gly Ala Pro Ala Trp Gln His Arg Gln 1135 1140 1145 1150	3638
CAC GTC TGC CTG CAC GCC CAC GCC CAC CTG CCA TTT TGC TGG GGG GCT His Val Cys Leu His Ala His Ala His Leu Pro Phe Cys Trp Gly Ala 1155 1160 1165	3686
GTC TGT CCT CAC CTT CCA CCC TGT GCC AGC CAC GGC TCC TGG CTC TCC Val Cys Pro His Leu Pro Pro Cys Ala Ser His Gly Ser Trp Leu Ser 1170 1175 1180	3734
GGG GCC TGG GGG CCT CTG GGG CAC AGG GGC AGG ACT CTG GGG CTG GGC Gly Ala Trp Gly Pro Leu Gly His Arg Gly Arg Thr Leu Gly Leu Gly 1185 1190 1195	3782
ACA GGC TAC AGA GAC AGT GGG GGA CTG GAC GAG ATC AGC AGG GTA GCC Thr Gly Tyr Arg Asp Ser Gly Gly Leu Asp Glu Ile Ser Arg Val Ala 1200 1205 1210	3830
CGT GGG ACG CAA GGC TTC CCG GGA CCC TGC ACC TGG AGA CGG ATC TCC Arg Gly Thr Gln Gly Phe Pro Gly Pro Cys Thr Trp Arg Arg Ile Ser 1215 1220 1225 1230	3878
AGT CTG GAG TCA GAA GTG TGAGTTATCA GCCACTCAGG CTCCGAGCCA Ser Leu Glu Ser Glu Val 1235	3926
GCTGGATTCT CTGCCTGCCA CTGTCAGGGT TAAGCGGCAG GCAGGATTGG GCTTTTCTGG	3986
CTTCTACCAT GAAATCCTGG CCATGGGACC CCAGTGACAG ATGATGTCTT CCATGGTCAT	4046
CAGTGACCTC AGTAGCCTCA AATCATGGTG AGGGCTGGGC TTTTGCTGTC CTCTTCTCAC	4106
GCAGAGTTCT GCCAGGAGGG TGTGCTGTGG GGGTCAGACT CCTGAGGCTC TCCCTTCCCT	4166
GGGGCTAGCC AGTTACTGGT CATGCCTGCT GTGGGCATGG AGGCTGGAAC TTGTGGTTGA	4226

GGCAGGGCCA TCCCGATCCT TGCTCTACCT GGCTAGAGTT TCTTCTCATC AGAGCACTGG 4286
 GACATTAAAC CCACCTTTTC CCAGAAAAAA AAAAAAAAAA AAAAAAAAAA AAAG 4340

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1236 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Gly Gly Ala Leu Gly Pro Ala Leu Leu Leu Thr Ser Leu Phe Gly
 1 5 10 15
 Ala Trp Ala Gly Leu Gly Pro Gly Gln Gly Glu Gln Gly Met Thr Val
 20 25 30
 Ala Val Val Phe Ser Ser Ser Gly Pro Pro Gln Ala Gln Phe Arg Val
 35 40 45
 Arg Leu Thr Pro Gln Ser Phe Leu Asp Leu Pro Leu Glu Ile Gln Pro
 50 55 60
 Leu Thr Val Gly Val Asn Thr Thr Asn Pro Ser Ser Leu Leu Thr Gln
 65 70 75 80
 Ile Cys Gly Leu Leu Gly Ala Ala His Val His Gly Ile Val Phe Glu
 85 90 95
 Asp Asn Val Asp Thr Glu Ala Val Ala Gln Ile Leu Asp Phe Ile Ser
 100 105 110
 Ser Gln Thr His Val Pro Ile Leu Ser Ile Ser Gly Gly Ser Ala Val
 115 120 125
 Val Leu Thr Pro Lys Glu Pro Gly Ser Ala Phe Leu Gln Leu Gly Val
 130 135 140
 Ser Leu Glu Gln Gln Leu Gln Val Leu Phe Lys Val Leu Glu Glu Tyr
 145 150 155 160
 Asp Trp Ser Ala Phe Ala Val Ile Thr Ser Leu His Pro Gly His Ala
 165 170 175
 Leu Phe Leu Glu Gly Val Arg Ala Val Ala Asp Ala Ser His Val Ser
 180 185 190
 Trp Arg Leu Leu Asp Val Val Thr Leu Glu Leu Asp Pro Gly Gly Pro
 195 200 205
 Arg Ala Arg Thr Gln Arg Leu Leu Arg Gln Leu Asp Ala Pro Val Phe
 210 215 220
 Val Ala Tyr Cys Ser Arg Glu Glu Ala Glu Val Leu Phe Ala Glu Ala
 225 230 235 240
 Ala Gln Ala Gly Leu Val Gly Pro Gly His Val Trp Leu Val Pro Asn
 245 250 255
 Leu Ala Leu Gly Ser Thr Asp Ala Pro Pro Ala Thr Phe Pro Val Gly
 260 265 270

Leu Ile Ser Val Val Thr Glu Ser Trp Arg Leu Ser Leu Arg Gln Lys
 275 280 285
 Val Arg Asp Gly Val Ala Ile Leu Ala Leu Gly Ala His Ser Tyr Trp
 290 295 300
 Arg Gln His Gly Thr Leu Pro Ala Pro Ala Gly Asp Cys Arg Val His
 305 310 315 320
 Pro Gly Pro Val Ser Pro Ala Arg Glu Ala Phe Tyr Arg His Leu Leu
 325 330 335
 Asn Val Thr Trp Glu Gly Arg Asp Phe Ser Phe Ser Pro Gly Gly Tyr
 340 345 350
 Leu Val Gln Pro Thr Met Val Val Ile Ala Leu Asn Arg His Arg Leu
 355 360 365
 Trp Glu Met Val Gly Arg Trp Glu His Gly Val Leu Tyr Met Lys Tyr
 370 375 380
 Pro Val Trp Pro Arg Tyr Ser Ala Ser Leu Gln Pro Val Val Asp Ser
 385 390 395 400
 Arg His Leu Thr Val Ala Thr Leu Glu Glu Arg Pro Phe Val Ile Val
 405 410 415
 Glu Ser Pro Asp Pro Gly Thr Gly Gly Cys Val Pro Asn Thr Val Pro
 420 425 430
 Cys Arg Arg Gln Ser Asn His Thr Phe Ser Ser Gly Asp Val Ala Pro
 435 440 445
 Tyr Thr Lys Leu Cys Cys Lys Gly Phe Cys Ile Asp Ile Leu Lys Lys
 450 455 460
 Leu Ala Arg Val Val Lys Phe Ser Tyr Asp Leu Tyr Leu Val Thr Asn
 465 470 475 480
 Gly Lys His Gly Lys Arg Val Arg Gly Val Trp Asn Gly Met Ile Gly
 485 490 495
 Glu Val Tyr Tyr Lys Arg Ala Asp Met Ala Ile Gly Ser Leu Thr Ile
 500 505 510
 Asn Glu Glu Arg Ser Glu Ile Val Asp Phe Ser Val Pro Phe Val Glu
 515 520 525
 Thr Gly Ile Ser Val Met Val Ala Arg Ser Asn Gly Thr Val Ser Pro
 530 535 540
 Ser Ala Phe Leu Glu Pro Tyr Ser Pro Ala Val Trp Val Met Met Phe
 545 550 555 560
 Val Met Cys Leu Thr Val Val Ala Ile Thr Val Phe Met Phe Glu Tyr
 565 570 575
 Phe Ser Pro Val Ser Tyr Asn Gln Asn Leu Thr Arg Gly Lys Lys Ser
 580 585 590
 Gly Gly Pro Ala Phe Thr Ile Gly Lys Ser Val Trp Leu Leu Trp Ala
 595 600 605
 Leu Val Phe Asn Asn Ser Val Pro Ile Glu Asn Pro Arg Gly Thr Thr
 610 615 620

Ser Lys Ile Met Val Leu Val Trp Ala Phe Phe Ala Val Ile Phe Leu
 625 630 635 640
 Ala Arg Tyr Thr Ala Asn Leu Ala Ala Phe Met Ile Gln Glu Gln Tyr
 645 650 655
 Ile Asp Thr Val Ser Gly Leu Ser Asp Lys Lys Phe Gln Arg Pro Gln
 660 665 670
 Asp Gln Tyr Pro Pro Phe Arg Phe Gly Thr Val Pro Asn Gly Ser Thr
 675 680 685
 Glu Arg Asn Ile Arg Ser Asn Tyr Arg Asp Met His Thr His Met Val
 690 695 700
 Lys Phe Asn Gln Arg Ser Val Glu Asp Ala Leu Thr Ser Leu Lys Met
 705 710 715 720
 Gly Lys Leu Asp Ala Phe Ile Tyr Asp Ala Ala Val Leu Asn Tyr Met
 725 730 735
 Ala Gly Lys Asp Glu Gly Cys Lys Leu Val Thr Ile Gly Ser Gly Lys
 740 745 750
 Val Phe Ala Thr Thr Gly Tyr Gly Ile Ala Met Gln Lys Asp Ser His
 755 760 765
 Trp Lys Arg Ala Ile Asp Leu Ala Leu Leu Gln Phe Leu Gly Asp Gly
 770 775 780
 Glu Thr Gln Lys Leu Glu Thr Val Trp Leu Ser Gly Ile Cys Gln Asn
 785 790 795 800
 Glu Lys Asn Glu Val Met Ser Ser Lys Leu Asp Ile Asp Asn Met Ala
 805 810 815
 Gly Val Phe Tyr Met Leu Leu Val Ala Met Gly Leu Ala Leu Leu Val
 820 825 830
 Phe Ala Trp Glu His Leu Val Tyr Trp Lys Leu Arg His Ser Val Pro
 835 840 845
 Asn Ser Ser Gln Leu Asp Phe Leu Leu Ala Phe Ser Arg Gly Ile Tyr
 850 855 860
 Ser Cys Phe Ser Gly Val Gln Ser Leu Ala Ser Pro Pro Arg Gln Ala
 865 870 875 880
 Ser Pro Asp Leu Thr Ala Ser Ser Ala Gln Ala Ser Val Leu Lys Met
 885 890 895
 Leu Gln Ala Ala Arg Asp Met Val Thr Thr Ala Gly Val Ser Ser Ser
 900 905 910
 Leu Asp Arg Ala Thr Arg Thr Ile Glu Asn Trp Gly Gly Gly Arg Arg
 915 920 925
 Ala Pro Pro Pro Ser Pro Cys Pro Thr Pro Arg Ser Gly Pro Ser Pro
 930 935 940
 Cys Leu Pro Thr Pro Asp Pro Pro Pro Glu Pro Ser Pro Thr Gly Trp
 945 950 955 960
 Gly Pro Pro Asp Gly Gly Arg Ala Ala Leu Val Arg Arg Ala Pro Gln
 965 970 975

Pro Pro Gly Arg Pro Pro Thr Pro Gly Pro Pro Leu Ser Asp Val Ser
 980 985 990
 Arg Val Ser Arg Arg Pro Ala Trp Glu Ala Arg Trp Pro Val Arg Thr
 995 1000 1005
 Gly His Cys Gly Arg His Leu Ser Ala Ser Glu Arg Pro Leu Ser Pro
 1010 1015 1020
 Ala Arg Cys His Tyr Ser Ser Phe Pro Arg Ala Asp Arg Ser Gly Arg
 1025 1030 1035 1040
 Pro Phe Leu Pro Leu Phe Pro Glu Pro Pro Glu Leu Glu Asp Leu Pro
 1045 1050 1055
 Leu Leu Gly Pro Glu Gln Leu Ala Arg Arg Glu Ala Leu Leu His Ala
 1060 1065 1070
 Ala Trp Ala Arg Gly Ser Arg Pro Arg His Ala Ser Leu Pro Ser Ser
 1075 1080 1085
 Val Ala Glu Ala Phe Ala Arg Pro Ser Ser Leu Pro Ala Gly Cys Thr
 1090 1095 1100
 Gly Pro Ala Cys Ala Arg Pro Asp Gly His Ser Ala Cys Arg Arg Leu
 1105 1110 1115 1120
 Ala Gln Ala Gln Ser Met Cys Leu Pro Ile Tyr Arg Glu Ala Cys Gln
 1125 1130 1135
 Glu Gly Glu Gln Ala Gly Ala Pro Ala Trp Gln His Arg Gln His Val
 1140 1145 1150
 Cys Leu His Ala His Ala His Leu Pro Phe Cys Trp Gly Ala Val Cys
 1155 1160 1165
 Pro His Leu Pro Pro Cys Ala Ser His Gly Ser Trp Leu Ser Gly Ala
 1170 1175 1180
 Trp Gly Pro Leu Gly His Arg Gly Arg Thr Leu Gly Leu Gly Thr Gly
 1185 1190 1195 1200
 Tyr Arg Asp Ser Gly Gly Leu Asp Glu Ile Ser Arg Val Ala Arg Gly
 1205 1210 1215
 Thr Gln Gly Phe Pro Gly Pro Cys Thr Trp Arg Arg Ile Ser Ser Leu
 1220 1225 1230
 Glu Ser Glu Val
 1235

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: both
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 2..22

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

C TCT GAG GCT CAG CCT GTC CCC AG
Ser Glu Ala Gln Pro Val Pro
1 5

24

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Ser Glu Ala Gln Pro Val Pro
1 5

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

AGAAGGGGGT G

11

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4808 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 311..4705

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

ATCATGGGAC CGGGTGAGCG CTGAGAATCG CGGCCGCAGC CATCAGCCCT GGAGATGACC	60
AGGAGCGGCC ACTGCTGAGA ACTATGTGGA GAGAGGCTGC GAGCCCTGCT GCAGAGCCTC	120
CGGCTGGGAT AGCCGCCCCC CGTGGGGGCG ATGCGGACAG CGCGGGACAG CCAGGGGAGC	180
GCGCTGGGGC CGCAGCATGC GGGAAACCCGC TAAACCCGGT GGCTGCTGAG GCGGCCGAGA	240
TGCTCGTGCG CGCAGCGCGC CCCACTGCAT CCTCGACCTT CTCGGGCTAC AGGGACCGTC	300

AGTGGCGACT	ATG	GGC	AGA	GTG	GGC	TAT	TGG	ACC	CTG	CTG	GTG	CTG	CCG		349
Met	Gly	Arg	Val	Gly	Tyr	Trp	Thr	Leu	Leu	Val	Leu	Pro			
1				5						10					
GCC	CTT	CTG	GTC	TGG	CGC	GGT	CCG	GGC	CCG	AGC	GGC	GGC	GAG	AAG	397
Ala	Leu	Leu	Val	Trp	Arg	Gly	Pro	Ala	Pro	Ser	Ala	Ala	Ala	Glu	Lys
15						20				25					
GGT	CCC	CCC	GCG	CTA	AAT	ATT	GCG	GTG	ATG	CTG	GGT	CAC	AGC	CAC	GAC
Gly	Pro	Pro	Ala	Leu	Asn	Ile	Ala	Val	Met	Leu	Gly	His	Ser	His	Asp
30					35				40					45	445
GTG	ACA	GAG	CGC	GAA	CTT	CGA	ACA	CTG	TGG	GGC	CCC	GAG	CAG	GCG	GCG
Val	Thr	Glu	Arg	Glu	Leu	Arg	Thr	Leu	Trp	Gly	Pro	Glu	Gln	Ala	Ala
			50						55					60	493
GGG	CTG	CCC	CTG	GAC	GTG	AAC	GTG	GTA	GCT	CTG	CTG	ATG	AAC	CGC	ACC
Gly	Leu	Pro	Leu	Asp	Val	Asn	Val	Val	Ala	Leu	Leu	Met	Asn	Arg	Thr
			65				70						75		541
GAC	CCC	AAG	AGC	CTC	ATC	ACG	CAC	GTG	TGC	GAC	CTC	ATG	TCC	GGG	GCA
Asp	Pro	Lys	Ser	Leu	Ile	Thr	His	Val	Cys	Asp	Leu	Met	Ser	Gly	Ala
		80					85					90			589
CGC	ATC	CAC	GGC	CTC	GTG	TTT	GGG	GAC	GAC	ACG	GAC	CAG	GAG	GCC	GTA
Arg	Ile	His	Gly	Leu	Val	Phe	Gly	Asp	Asp	Thr	Asp	Gln	Glu	Ala	Val
	95					100					105				637
GCC	CAG	ATG	CTG	GAT	TTT	ATC	TCC	TCC	CAC	ACC	TTC	GTC	CCC	ATC	TTG
Ala	Gln	Met	Leu	Asp	Phe	Ile	Ser	Ser	His	Thr	Phe	Val	Pro	Ile	Leu
110					115					120				125	685
GGC	ATT	CAT	GGG	GGC	GCA	TCT	ATG	ATC	ATG	GCT	GAC	AAG	GAT	CCG	ACG
Gly	Ile	His	Gly	Gly	Ala	Ser	Met	Ile	Met	Ala	Asp	Lys	Asp	Pro	Thr
			130						135					140	733
TCT	ACC	TTC	TTC	CAG	TTT	GGA	GCG	TCC	ATC	CAG	CAG	CAA	GCC	ACG	GTC
Ser	Thr	Phe	Phe	Gln	Phe	Gly	Ala	Ser	Ile	Gln	Gln	Gln	Ala	Thr	Val
			145					150					155		781
ATG	CTG	AAG	ATC	ATG	CAG	GAT	TAT	GAC	TGG	CAT	GTC	TTC	TCC	CTG	GTG
Met	Leu	Lys	Ile	Met	Gln	Asp	Tyr	Asp	Trp	His	Val	Phe	Ser	Leu	Val
		160					165					170			829
ACC	ACT	ATC	TTC	CCT	GGC	TAC	AGG	GAA	TTC	ATC	AGC	TTC	GTC	AAG	ACC
Thr	Thr	Ile	Phe	Pro	Gly	Tyr	Arg	Glu	Phe	Ile	Ser	Phe	Val	Lys	Thr
	175					180					185				877
ACA	GTG	GAC	AAC	AGC	TTT	GTG	GGC	TGG	GAC	ATG	CAG	AAT	GTG	ATC	ACA
Thr	Val	Asp	Asn	Ser	Phe	Val	Gly	Trp	Asp	Met	Gln	Asn	Val	Ile	Thr
190					195					200				205	925
CTG	GAC	ACT	TCC	TTT	GAG	GAT	GCA	AAG	ACA	CAA	GTC	CAG	CTG	AAG	AAG
Leu	Asp	Thr	Ser	Phe	Glu	Asp	Ala	Lys	Thr	Gln	Val	Gln	Leu	Lys	Lys
				210				215					220		973
ATC	CAC	TCT	TCT	GTC	ATC	TTG	CTC	TAC	TGT	TCC	AAA	GAC	GAG	GCT	GTT
Ile	His	Ser	Ser	Val	Ile	Leu	Leu	Tyr	Cys	Ser	Lys	Asp	Glu	Ala	Val
			225				230						235		1021
CTC	ATT	CTG	AGT	GAG	GCC	CGC	TCC	CTT	GGC	CTC	ACC	GGG	TAT	GAT	TTC
Leu	Ile	Leu	Ser	Glu	Ala	Arg	Ser	Leu	Gly	Leu	Thr	Gly	Tyr	Asp	Phe
		240					245					250			1069
TTC	TGG	ATT	GTC	CCC	AGC	TTG	GTC	TCT	GGG	AAC	ACG	GAG	CTC	ATC	CCA
Phe	Trp	Ile	Val	Pro	Ser	Leu	Val	Ser	Gly	Asn	Thr	Glu	Leu	Ile	Pro
	255					260					265				1117

AAA Lys 270	GAG Glu	TTT Phe	CCA Pro	TCG Ser	GGA Gly 275	CTC Leu	ATT Ile	TCT Ser	GTC Val	TCC Ser 280	TAC Tyr	GAT Asp	GAC Asp	TGG Trp 285	GAC Asp	1165
TAC Tyr	AGC Ser	CTG Leu	GAG Glu	GCG Ala 290	AGA Arg	GTG Val	AGG Arg	GAC Asp	GGC Gly 295	ATT Ile	GGC Gly	ATC Ile	CTA Leu	ACC Thr 300	ACC Thr	1213
GCT Ala	GCA Ala	TCT Ser	TCT Ser 305	ATG Met	CTG Leu	GAG Glu	AAG Lys	TTC Phe 310	TCC Ser	TAC Tyr	ATC Ile	CCC Pro	GAG Glu 315	GCC Ala	AAG Lys	1261
GCC Ala	AGC Ser	TGC Cys 320	TAC Tyr	GGG Gly	CAG Gln	ATG Met	GAG Glu 325	AGG Arg	CCA Pro	GAG Glu	GTC Val	CCG Pro 330	ATG Met	CAC His	ACC Thr	1309
TTG Leu 335	CAC His	CCA Pro	TTT Phe	ATG Met	GTC Val	AAT Asn 340	GTT Val	ACA Thr	TGG Trp	GAT Asp	GGC Gly 345	AAA Lys	GAC Asp	TTA Leu	TCC Ser	1357
TTC Phe 350	ACT Thr	GAG Glu	GAA Glu	GGC Gly 355	TAC Tyr	CAG Gln	GTG Val	CAC His	CCC Pro 360	AGG Arg	CTG Leu	GTG Val	GTG Val	ATT Ile	GTG Val 365	1405
CTG Leu	AAC Asn	AAA Lys	GAC Asp	CGG Arg 370	GAA Glu	TGG Trp	GAA Glu	AAG Lys	GTG Val 375	GGC Gly	AAG Lys	TGG Trp	GAG Glu	AAC Asn 380	CAT His	1453
ACG Thr	CTG Leu	AGC Ser	CTG Leu 385	AGG Arg	CAC His	GCC Ala	GTG Val	TGG Trp 390	CCC Pro	AGG Arg	TAC Tyr	AAG Lys	TCC Ser 395	TTC Phe	TCC Ser	1501
GAC Asp	TGT Cys	GAG Glu	CCG Pro 400	GAT Asp	GAC Asp	AAC Asn	CAT His 405	CTC Leu	AGC Ser	ATC Ile	GTC Val	ACC Thr 410	CTG Leu	GAG Glu	GAG Glu	1549
GCC Ala 415	CCA Pro	TTC Phe	GTC Val	ATC Ile	GTG Val	GAA Glu 420	GAC Asp	ATA Ile	GAC Asp	CCC Pro	CTG Leu 425	ACC Thr	GAG Glu	ACG Thr	TGT Cys	1597
GTG Val 430	AGG Arg	AAC Asn	ACC Thr	GTG Val	CCA Pro	TGT Cys 435	CGG Arg	AAG Lys	TTC Phe	GTC Val 440	AAA Lys	ATC Ile	AAC Asn	AAT Asn	TCA Ser 445	1645
ACC Thr	AAT Asn	GAG Glu	GGG Gly 450	ATG Met	AAT Asn	GTG Val	AAG Lys	AAA Lys	TGC Cys 455	TGC Cys	AAG Lys	GGG Gly	TTC Phe	TGC Cys 460	ATT Ile	1693
GAT Asp	ATT Ile	CTG Leu	AAG Lys 465	AAG Lys	CTT Leu	TCC Ser	AGA Arg	ACT Thr 470	GTG Val	AAG Lys	TTT Phe	ACT Thr	TAC Tyr 475	GAC Asp	CTC Leu	1741
TAT Tyr	CTG Leu	GTG Val	ACC Thr 480	AAT Asn	GGG Gly	AAG Lys	CAT His 485	GGC Gly	AAG Lys	AAA Lys	GTT Val	AAC Asn 490	AAT Asn	GTG Val	TGG Trp	1789
AAT Asn 495	GGA Gly	ATG Met	ATC Ile	GGT Gly	GAA Glu	GTG Val	GTC Val	TAT Tyr	CAA Gln	CGG Arg	GCA Ala 505	GTC Val	ATG Met	GCA Ala	GTT Val	1837
GGC Gly 510	TCG Ser	CTC Leu	ACC Thr	ATC Ile	AAT Asn 515	GAG Glu	GAA Glu	CGT Arg	TCT Ser	GAA Glu 520	GTG Val	GTG Val	GAC Asp	TTC Phe	TCT Ser 525	1885
GTG Val	CCC Pro	TTT Phe	GTG Val	GAA Glu 530	ACG Thr	GGA Gly	ATC Ile	AGT Ser	GTC Val 535	ATG Met	GTT Val	TCA Ser	AGA Arg	AGT Ser	AAT Asn 540	1933

GGC ACC GTC TCA CCT TCT GCT TTT CTA GAA CCA TTC AGC GCC TCT GTC	1981
Gly Thr Val Ser Pro Ser Ala Phe Leu Glu Pro Phe Ser Ala Ser Val	
545 550 555	
TGG GTG ATG ATG TTT GTG ATG CTG CTC ATT GTT TCT GCC ATA GCT GTT	2029
Trp Val Met Met Phe Val Met Leu Leu Ile Val Ser Ala Ile Ala Val	
560 565 570	
TGG GTC TTG GAT TAC TCC AGC CCT GTT GGA TAC AAC AGA AAC TTA GCC	2077
Trp Val Leu Asp Tyr Ser Ser Pro Val Gly Tyr Asn Arg Asn Leu Ala	
575 580 585	
AAA GGG AAA GCA CCC CAT GGG CCT TCT TTT ACA ATT GGA AAA GCT ATA	2125
Lys Gly Lys Ala Pro His Gly Pro Ser Phe Thr Ile Gly Lys Ala Ile	
590 595 600 605	
TGG CTT CTT TGG GGC CTG GTG TTC AAT AAC TCC GTG CCT GTC CAG AAT	2173
Trp Leu Leu Trp Gly Leu Val Phe Asn Asn Ser Val Pro Val Gln Asn	
610 615 620	
CCT AAA GGG ACC ACC AGC AAG ATC ATG GTA TCT GTA TGG GCC TTC TTC	2221
Pro Lys Gly Thr Ser Lys Ile Met Val Ser Val Trp Ala Phe Phe	
625 630 635	
GCT GTC ATA TTC CTG GCT AGC TAC ACA GCC AAT CTG GCT GCC TTC ATG	2269
Ala Val Ile Phe Leu Ala Ser Tyr Thr Ala Asn Leu Ala Ala Phe Met	
640 645 650	
ATC CAA GAG GAA TTT GTG GAC CAA GTG ACC GGC CTC AGT GAC AAA AAG	2317
Ile Gln Glu Glu Phe Val Asp Gln Val Thr Gly Leu Ser Asp Lys Lys	
655 660 665	
TTT CAG AGA CCT CAT GAC TAT TCC CCA CCT TTT CGA TTT GGG ACA GTG	2365
Phe Gln Arg Pro His Asp Tyr Ser Pro Pro Phe Arg Phe Gly Thr Val	
670 675 680 685	
CCT AAT GGA AGC ACG GAG AGA AAC ATT CGG AAT AAC TAT CCC TAC ATG	2413
Pro Asn Gly Ser Thr Glu Arg Asn Ile Arg Asn Asn Tyr Pro Tyr Met	
690 695 700	
CAT CAG TAC ATG ACC AAA TTT AAT CAG AAA GGA GTA GAG GAC GCC TTG	2461
His Gln Tyr Met Thr Lys Phe Asn Gln Lys Gly Val Glu Asp Ala Leu	
705 710 715	
GTC AGC CTG AAA ACG GGG AAG CTG GAC GCT TTC ATC TAC GAT GCC GCA	2509
Val Ser Leu Lys Thr Gly Lys Leu Asp Ala Phe Ile Tyr Asp Ala Ala	
720 725 730	
GTC TTG AAT TAC AAG GCT GGG AGG GAT GAA GGC TGC AAG CTG GTG ACC	2557
Val Leu Asn Tyr Lys Ala Gly Arg Asp Glu Gly Cys Lys Leu Val Thr	
735 740 745	
ATC GGG AGT GGG TAC ATC TTT GCC ACC ACC GGT TAT GGA ATT GCC CTT	2605
Ile Gly Ser Gly Tyr Ile Phe Ala Thr Thr Gly Tyr Gly Ile Ala Leu	
750 755 760 765	
CAG AAA GGC TCT CCT TGG AAG AGG CAG ATC GAC CTG GCC TTG CTT CAG	2653
Gln Lys Gly Ser Pro Trp Lys Arg Gln Ile Asp Leu Ala Leu Leu Gln	
770 775 780	
TTT GTG GGT GAT GGT GAG ATG GAG GAG CTG GAG ACC CTG TGG CTC ACT	2701
Phe Val Gly Asp Gly Glu Met Glu Glu Leu Glu Thr Leu Trp Leu Thr	
785 790 795	
GGG ATC TGC CAC AAC GAG AAG AAC GAG GTG ATG AGC AGC CAG CTG GAC	2749
Gly Ile Cys His Asn Glu Lys Asn Glu Val Met Ser Ser Gln Leu Asp	
800 805 810	

ATT Ile 815	GAC Asp	AAC Asn	ATG Met	GCG Ala	GGC Gly	GTA Val 820	TTC Phe	TAC Tyr	ATG Met	CTG Leu	GCT Ala 825	GCC Ala	GCC Ala	ATG Met	GCC Ala	2797
CTT Leu 830	AGC Ser	CTC Leu	ATC Ile	ACC Thr	TTC Phe 835	ATC Ile	TGG Trp	GAG Glu	CAC His	CTC Leu 840	TTC Phe	TAC Tyr	TGG Trp	AAG Lys	CTG Leu 845	2845
CGC Arg	TTC Phe	TGT Cys	TTC Phe	ACG Thr 850	GGC Gly	GTG Val	TGC Cys	TCC Ser	GAC Asp 855	CGG Arg	CCT Pro	GGG Gly	TTG Leu	CTC Leu 860	TTC Phe	2893
TCC Ser	ATC Ile	AGC Ser	AGG Arg 865	GGC Gly	ATC Ile	TAC Tyr	AGC Ser	TGC Cys 870	ATT Ile	CAT His	GGA Gly	GTG Val	CAC His 875	ATT Ile	GAA Glu	2941
GAA Glu	AAG Lys	AAG Lys 880	AAG Lys	TCT Ser	CCA Pro	GAC Asp	TTC Phe 885	AAT Asn	CTG Leu	ACG Thr	GGA Gly 890	TCC Ser	CAG Gln	AGC Ser	AAC Asn	2989
ATG Met 895	TTA Leu	AAA Lys	CTC Leu	CTC Leu	CGG Arg	TCA Ser 900	GCC Ala	AAA Lys	AAC Asn	ATT Ile	TCC Ser 905	AGC Ser	ATG Met	TCC Ser	AAC Asn	3037
ATG Met 910	AAC Asn	TCC Ser	TCA Ser	AGA Arg	ATG Met 915	GAC Asp	TCA Ser	CCC Pro	AAA Lys	AGA Arg 920	GCT Ala	GCT Ala	GAC Asp	TTC Phe	ATC Ile 925	3085
CAA Gln	AGA Arg	GGT Gly	TCC Ser	CTC Leu 930	ATC Ile	ATG Met	GAC Asp	ATG Met	GTT Val 935	TCA Ser	GAT Asp	AAG Lys	GGG Gly	AAT Asn 940	TTG Leu	3133
ATG Met	TAC Tyr	TCA Ser	GAC Asp 945	AAC Asn	AGG Arg	TCC Ser	TTT Phe	CAG Gln 950	GGG Gly	AAA Lys	GAG Glu	AGC Ser	ATT Ile 955	TTT Phe	GGA Gly	3181
GAC Asp	AAC Asn	ATG Met	AAC Asn	GAA Glu 960	CTC Leu	CAA Gln	ACA Thr 965	TTT Phe	GTG Val	GCC Ala	AAC Asn	CGG Arg 970	CAG Gln	AAG Lys	GAT Asp	3229
AAC Asn 975	CTC Leu	AAT Asn	AAC Asn	TAT Tyr	GTA Val	TTC Phe 980	CAG Gln	GGA Gly	CAA Gln	CAT His	CCT Pro 985	CTT Leu	ACT Thr	CTC Leu	AAT Asn	3277
GAG Glu 990	TCC Ser	AAC Asn	CCT Pro	AAC Asn	ACG Thr 995	GTG Val	GAG Glu	GTG Val	GCC Ala	GTG Val 1000	AGC Ser	ACA Thr	GAA Glu	TCC Ser	AAA Lys 1005	3325
GCG Ala	AAC Asn	TCT Ser	AGA Arg	CCC Pro 1010	CGG Gln	CAG Leu	CTG Trp	TGG Lys	AAG Lys 1015	AAA Lys	TCC Ser	GTG Val	GAT Asp	TCC Ser 1020	ATA Ile	3373
CGC Arg	CAG Gln	GAT Asp	TCA Ser 1025	CTA Leu	TCC Ser	CAG Gln	AAT Asn	CCA Pro 1030	GTC Val	TCC Ser	CAG Gln	AGG Arg	GAT Asp 1035	GAG Glu	GCA Ala	3421
ACA Thr 1040	GCA Ala	GAG Glu	AAT Asn	AGG Arg	ACC Thr	CAC His	TCC Ser 1045	CTA Leu	AAG Lys	AGC Ser	CCT Pro 1050	AGG Arg	TAT Tyr	CTT Leu	CCA Pro	3469
GAA Glu 1055	GAG Glu	ATG Met	GCC Ala	CAC His	TCT Ser	GAC Asp 1060	ATT Ile	TCA Ser	GAA Glu	ACG Thr	TCA Ser 1065	AAT Asn	CGG Arg	GCC Ala	ACG Thr	3517
TGC Cys 1070	CAC His	AGG Arg	GAA Glu	CCT Pro	GAC Asp 1075	AAC Asn	AGT Ser	AAG Lys	AAC Asn	CAC His 1080	AAA Lys	ACC Thr	AAG Lys	GAC Asp	AAC Asn 1085	3565

TTT AAA AGG TCA GTG GCC TCC AAA TAC CCC AAG GAC TGT AGT GAG GTC Phe Lys Arg Ser Val Ala Ser Lys Tyr Pro Lys Asp Cys Ser Glu Val 1090 1095 1100	3613
GAG CGC ACC TAC CTG AAA ACC AAA TCA AGC TCC CCT AGA GAC AAG ATC Glu Arg Thr Tyr Leu Lys Thr Lys Ser Ser Ser Pro Arg Asp Lys Ile 1105 1110 1115	3661
TAC ACT ATA GAT GGT GAG AAG GAG CCT GGT TTC CAC TTA GAT CCA CCC Tyr Thr Ile Asp Gly Glu Lys Glu Pro Gly Phe His Leu Asp Pro Pro 1120 1125 1130	3709
CAG TTT GTT GAA AAT GTG ACC CTG CCC GAG AAC GTG GAC TTC CCG GAC Gln Phe Val Glu Asn Val Thr Leu Pro Glu Asn Val Asp Phe Pro Asp 1135 1140 1145	3757
CCC TAC CAG GAT CCC AGT GAA AAC TTC CGC AAG GGG GAC TCC ACG CTG Pro Tyr Gln Asp Pro Ser Glu Asn Phe Arg Lys Gly Asp Ser Thr Leu 1150 1155 1160 1165	3805
CCA ATG AAC CGG AAC CCC TTG CAT AAT GAA GAG GGG CTT TCC AAC AAC Pro Met Asn Arg Asn Pro Leu His Asn Glu Glu Gly Leu Ser Asn Asn 1170 1175 1180	3853
GAC CAG TAT AAA CTC TAC TCC AAG CAC TTC ACC TTG AAA GAC AAG GGT Asp Gln Tyr Lys Leu Tyr Ser Lys His Phe Thr Leu Lys Asp Lys Gly 1185 1190 1195	3901
TCC CCG CAC AGT GAG ACC AGC GAG CGA TAC CGG CAG AAC TCC ACG CAC Ser Pro His Ser Glu Thr Ser Glu Arg Tyr Arg Gln Asn Ser Thr His 1200 1205 1210	3949
TGC AGA AGC TGC CTT TCC AAC ATG CCC ACC TAT TCA GGC CAC TTC ACC Cys Arg Ser Cys Leu Ser Asn Met Pro Thr Tyr Ser Gly His Phe Thr 1215 1220 1225	3997
ATG AGG TCC CCC TTC AAG TGC GAT GCC TGC CTG CGG ATG GGG AAC CTC Met Arg Ser Pro Phe Lys Cys Asp Ala Cys Leu Arg Met Gly Asn Leu 1230 1235 1240 1245	4045
TAT GAC ATC GAT GAA GAC CAG ATG CTT CAG GAG ACA GGT AAC CCA GCC Tyr Asp Ile Asp Glu Asp Gln Met Leu Gln Glu Thr Gly Asn Pro Ala 1250 1255 1260	4093
ACC GGG GAG CAG GTC TAC CAG CAG GAC TGG GCA CAG AAC AAT GCC CTT Thr Gly Glu Gln Val Tyr Gln Gln Asp Trp Ala Gln Asn Asn Ala Leu 1265 1270 1275	4141
CAA TTA CAA AAG AAC AAG CTA AGG ATT AGC CGT CAG CAT TCC TAC GAT Gln Leu Gln Lys Asn Lys Leu Arg Ile Ser Arg Gln His Ser Tyr Asp 1280 1285 1290	4189
AAC ATT GTC GAC AAA CCT AGG GAG CTA GAC CTT AGC AGG CCC TCC CGG Asn Ile Val Asp Lys Pro Arg Glu Leu Asp Leu Ser Arg Pro Ser Arg 1295 1300 1305	4237
AGC ATA AGC CTC AAG GAC AGG GAA CGG CTT CTG GAG GGA AAT TTT TAC Ser Ile Ser Leu Lys Asp Arg Glu Arg Leu Leu Glu Gly Asn Phe Tyr 1310 1315 1320 1325	4285
GGC AGC CTG TTT AGT GTC CCC TCA AGC AAA CTC TCG GGG AAA AAA AGC Gly Ser Leu Phe Ser Val Pro Ser Ser Lys Leu Ser Gly Lys Lys Ser 1330 1335 1340	4333
TCC CTT TTC CCC CAA GGT CTG GAG GAC AGC AAG AGG AGC AAG TCT CTC Ser Leu Phe Pro Gln Gly Leu Glu Asp Ser Lys Arg Ser Lys Ser Leu 1345 1350 1355	4381

TTG CCA GAC CAC ACC TCC GAT AAC CCT TTC CTC CAC TCC CAC AGG GAT Leu Pro Asp His Thr Ser Asp Asn Pro Phe Leu His Ser His Arg Asp 1360 1365 1370	4429
GAC CAA CGC TTG GTT ATT GGG AGA TGC CCC TCG GAC CCT TAC AAA CAC Asp Gln Arg Leu Val Ile Gly Arg Cys Pro Ser Asp Pro Tyr Lys His 1375 1380 1385	4477
TCG TTG CCA TCC CAG GCG GTG AAT GAC AGC TAT CTT CGG TCG TCC TTG Ser Leu Pro Ser Gln Ala Val Asn Asp Ser Tyr Leu Arg Ser Ser Leu 1390 1395 1400 1405	4525
AGG TCA ACG GCA TCG TAC TGT TCC AGG GAC AGT CGG GGC CAC AAT GAT Arg Ser Thr Ala Ser Tyr Cys Ser Arg Asp Ser Arg Gly His Asn Asp 1410 1415 1420	4573
GTG TAT ATT TCG GAG CAT GTT ATG CCT TAT GCT GCA AAT AAG AAT AAT Val Tyr Ile Ser Glu His Val Met Pro Tyr Ala Ala Asn Lys Asn Asn 1425 1430 1435	4621
ATG TAC TCT ACC CCC AGG GTT TTA AAT TCC TGC AGC AAT AGA CGC GTG Met Tyr Ser Thr Pro Arg Val Leu Asn Ser Cys Ser Asn Arg Arg Val 1440 1445 1450	4669
TAC AAG GAA ATG CCT AGT ATC GAA TCT GAT GTT TAAAAATCTT CCATTAATGT Tyr Lys Glu Met Pro Ser Ile Glu Ser Asp Val 1455 1460 146	4722
TTTATCTATA GGGAAATACA CGTAATGGCC AATGTTCTGG AGGGTAAATG TTGGATGTCC	4782
AATAGTGCCC TGCTAAGAGG AAGGAG	4808

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1464 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met Gly Arg Val Gly Tyr Trp Thr Leu Leu Val Leu Pro Ala Leu Leu 1 5 10 15
Val Trp Arg Gly Pro Ala Pro Ser Ala Ala Ala Glu Lys Gly Pro Pro 20 25 30
Ala Leu Asn Ile Ala Val Met Leu Gly His Ser His Asp Val Thr Glu 35 40 45
Arg Glu Leu Arg Thr Leu Trp Gly Pro Glu Gln Ala Ala Gly Leu Pro 50 55 60
Leu Asp Val Asn Val Val Ala Leu Leu Met Asn Arg Thr Asp Pro Lys 65 70 75 80
Ser Leu Ile Thr His Val Cys Asp Leu Met Ser Gly Ala Arg Ile His 85 90 95
Gly Leu Val Phe Gly Asp Asp Thr Asp Gln Glu Ala Val Ala Gln Met 100 105 110
Leu Asp Phe Ile Ser Ser His Thr Phe Val Pro Ile Leu Gly Ile His 115 120 125

Gly Gly Ala Ser Met Ile Met Ala Asp Lys Asp Pro Thr Ser Thr Phe
 130 135 140
 Phe Gln Phe Gly Ala Ser Ile Gln Gln Gln Ala Thr Val Met Leu Lys
 145 150 155 160
 Ile Met Gln Asp Tyr Asp Trp His Val Phe Ser Leu Val Thr Thr Ile
 165 170 175
 Phe Pro Gly Tyr Arg Glu Phe Ile Ser Phe Val Lys Thr Thr Val Asp
 180 185 190
 Asn Ser Phe Val Gly Trp Asp Met Gln Asn Val Ile Thr Leu Asp Thr
 195 200 205
 Ser Phe Glu Asp Ala Lys Thr Gln Val Gln Leu Lys Lys Ile His Ser
 210 215 220
 Ser Val Ile Leu Leu Tyr Cys Ser Lys Asp Glu Ala Val Leu Ile Leu
 225 230 235 240
 Ser Glu Ala Arg Ser Leu Gly Leu Thr Gly Tyr Asp Phe Phe Trp Ile
 245 250 255
 Val Pro Ser Leu Val Ser Gly Asn Thr Glu Leu Ile Pro Lys Glu Phe
 260 265 270
 Pro Ser Gly Leu Ile Ser Val Ser Tyr Asp Asp Trp Asp Tyr Ser Leu
 275 280 285
 Glu Ala Arg Val Arg Asp Gly Ile Gly Ile Leu Thr Thr Ala Ala Ser
 290 295 300
 Ser Met Leu Glu Lys Phe Ser Tyr Ile Pro Glu Ala Lys Ala Ser Cys
 305 310 315 320
 Tyr Gly Gln Met Glu Arg Pro Glu Val Pro Met His Thr Leu His Pro
 325 330 335
 Phe Met Val Asn Val Thr Trp Asp Gly Lys Asp Leu Ser Phe Thr Glu
 340 345 350
 Glu Gly Tyr Gln Val His Pro Arg Leu Val Val Ile Val Leu Asn Lys
 355 360 365
 Asp Arg Glu Trp Glu Lys Val Gly Lys Trp Glu Asn His Thr Leu Ser
 370 375 380
 Leu Arg His Ala Val Trp Pro Arg Tyr Lys Ser Phe Ser Asp Cys Glu
 385 390 395 400
 Pro Asp Asp Asn His Leu Ser Ile Val Thr Leu Glu Glu Ala Pro Phe
 405 410 415
 Val Ile Val Glu Asp Ile Asp Pro Leu Thr Glu Thr Cys Val Arg Asn
 420 425 430
 Thr Val Pro Cys Arg Lys Phe Val Lys Ile Asn Asn Ser Thr Asn Glu
 435 440 445
 Gly Met Asn Val Lys Lys Cys Cys Lys Gly Phe Cys Ile Asp Ile Leu
 450 455 460
 Lys Lys Leu Ser Arg Thr Val Lys Phe Thr Tyr Asp Leu Tyr Leu Val
 465 470 475 480

Thr Asn Gly Lys His Gly Lys Lys Val Asn Asn Val Trp Asn Gly Met
 485 490 495
 Ile Gly Glu Val Val Tyr Gln Arg Ala Val Met Ala Val Gly Ser Leu
 500 505 510
 Thr Ile Asn Glu Glu Arg Ser Glu Val Val Asp Phe Ser Val Pro Phe
 515 520 525
 Val Glu Thr Gly Ile Ser Val Met Val Ser Arg Ser Asn Gly Thr Val
 530 535 540
 Ser Pro Ser Ala Phe Leu Glu Pro Phe Ser Ala Ser Val Trp Val Met
 545 550 555 560
 Met Phe Val Met Leu Leu Ile Val Ser Ala Ile Ala Val Trp Val Leu
 565 570 575
 Asp Tyr Ser Ser Pro Val Gly Tyr Asn Arg Asn Leu Ala Lys Gly Lys
 580 585 590
 Ala Pro His Gly Pro Ser Phe Thr Ile Gly Lys Ala Ile Trp Leu Leu
 595 600 605
 Trp Gly Leu Val Phe Asn Asn Ser Val Pro Val Gln Asn Pro Lys Gly
 610 615 620
 Thr Thr Ser Lys Ile Met Val Ser Val Trp Ala Phe Phe Ala Val Ile
 625 630 635 640
 Phe Leu Ala Ser Tyr Thr Ala Asn Leu Ala Ala Phe Met Ile Gln Glu
 645 650 655
 Glu Phe Val Asp Gln Val Thr Gly Leu Ser Asp Lys Lys Phe Gln Arg
 660 665 670
 Pro His Asp Tyr Ser Pro Pro Phe Arg Phe Gly Thr Val Pro Asn Gly
 675 680 685
 Ser Thr Glu Arg Asn Ile Arg Asn Asn Tyr Pro Tyr Met His Gln Tyr
 690 695 700
 Met Thr Lys Phe Asn Gln Lys Gly Val Glu Asp Ala Leu Val Ser Leu
 705 710 715 720
 Lys Thr Gly Lys Leu Asp Ala Phe Ile Tyr Asp Ala Ala Val Leu Asn
 725 730 735
 Tyr Lys Ala Gly Arg Asp Glu Gly Cys Lys Leu Val Thr Ile Gly Ser
 740 745 750
 Gly Tyr Ile Phe Ala Thr Thr Gly Tyr Gly Ile Ala Leu Gln Lys Gly
 755 760 765
 Ser Pro Trp Lys Arg Gln Ile Asp Leu Ala Leu Leu Gln Phe Val Gly
 770 775 780
 Asp Gly Glu Met Glu Glu Leu Glu Thr Leu Trp Leu Thr Gly Ile Cys
 785 790 795 800
 His Asn Glu Lys Asn Glu Val Met Ser Ser Gln Leu Asp Ile Asp Asn
 805 810 815
 Met Ala Gly Val Phe Tyr Met Leu Ala Ala Met Ala Leu Ser Leu
 820 825 830

Ile Thr Phe Ile Trp Glu His Leu Phe Tyr Trp Lys Leu Arg Phe Cys
 835 840 845
 Phe Thr Gly Val Cys Ser Asp Arg Pro Gly Leu Leu Phe Ser Ile Ser
 850 855 860
 Arg Gly Ile Tyr Ser Cys Ile His Gly Val His Ile Glu Glu Lys Lys
 865 870 875 880
 Lys Ser Pro Asp Phe Asn Leu Thr Gly Ser Gln Ser Asn Met Leu Lys
 885 890 895
 Leu Leu Arg Ser Ala Lys Asn Ile Ser Ser Met Ser Asn Met Asn Ser
 900 905 910
 Ser Arg Met Asp Ser Pro Lys Arg Ala Ala Asp Phe Ile Gln Arg Gly
 915 920 925
 Ser Leu Ile Met Asp Met Val Ser Asp Lys Gly Asn Leu Met Tyr Ser
 930 935 940
 Asp Asn Arg Ser Phe Gln Gly Lys Glu Ser Ile Phe Gly Asp Asn Met
 945 950 955 960
 Asn Glu Leu Gln Thr Phe Val Ala Asn Arg Gln Lys Asp Asn Leu Asn
 965 970 975
 Asn Tyr Val Phe Gln Gly Gln His Pro Leu Thr Leu Asn Glu Ser Asn
 980 985 990
 Pro Asn Thr Val Glu Val Ala Val Ser Thr Glu Ser Lys Ala Asn Ser
 995 1000 1005
 Arg Pro Arg Gln Leu Trp Lys Lys Ser Val Asp Ser Ile Arg Gln Asp
 1010 1015 1020
 Ser Leu Ser Gln Asn Pro Val Ser Gln Arg Asp Glu Ala Thr Ala Glu
 1025 1030 1035 1040
 Asn Arg Thr His Ser Leu Lys Ser Pro Arg Tyr Leu Pro Glu Glu Met
 1045 1050 1055
 Ala His Ser Asp Ile Ser Glu Thr Ser Asn Arg Ala Thr Cys His Arg
 1060 1065 1070
 Glu Pro Asp Asn Ser Lys Asn His Lys Thr Lys Asp Asn Phe Lys Arg
 1075 1080 1085
 Ser Val Ala Ser Lys Tyr Pro Lys Asp Cys Ser Glu Val Glu Arg Thr
 1090 1095 1100
 Tyr Leu Lys Thr Lys Ser Ser Ser Pro Arg Asp Lys Ile Tyr Thr Ile
 1105 1110 1115 1120
 Asp Gly Glu Lys Glu Pro Gly Phe His Leu Asp Pro Pro Gln Phe Val
 1125 1130 1135
 Glu Asn Val Thr Leu Pro Glu Asn Val Asp Phe Pro Asp Pro Tyr Gln
 1140 1145 1150
 Asp Pro Ser Glu Asn Phe Arg Lys Gly Asp Ser Thr Leu Pro Met Asn
 1155 1160 1165
 Arg Asn Pro Leu His Asn Glu Glu Gly Leu Ser Asn Asn Asp Gln Tyr
 1170 1175 1180

Lys Leu Tyr Ser Lys His Phe Thr Leu Lys Asp Lys Gly Ser Pro His
 1185 1190 1195 1200
 Ser Glu Thr Ser Glu Arg Tyr Arg Gln Asn Ser Thr His Cys Arg Ser
 1205 1210 1215
 Cys Leu Ser Asn Met Pro Thr Tyr Ser Gly His Phe Thr Met Arg Ser
 1220 1225 1230
 Pro Phe Lys Cys Asp Ala Cys Leu Arg Met Gly Asn Leu Tyr Asp Ile
 1235 1240 1245
 Asp Glu Asp Gln Met Leu Gln Glu Thr Gly Asn Pro Ala Thr Gly Glu
 1250 1255 1260
 Gln Val Tyr Gln Gln Asp Trp Ala Gln Asn Asn Ala Leu Gln Leu Gln
 1265 1270 1275 1280
 Lys Asn Lys Leu Arg Ile Ser Arg Gln His Ser Tyr Asp Asn Ile Val
 1285 1290 1295
 Asp Lys Pro Arg Glu Leu Asp Leu Ser Arg Pro Ser Arg Ser Ile Ser
 1300 1305 1310
 Leu Lys Asp Arg Glu Arg Leu Leu Glu Gly Asn Phe Tyr Gly Ser Leu
 1315 1320 1325
 Phe Ser Val Pro Ser Ser Lys Leu Ser Gly Lys Lys Ser Ser Leu Phe
 1330 1335 1340
 Pro Gln Gly Leu Glu Asp Ser Lys Arg Ser Lys Ser Leu Leu Pro Asp
 1345 1350 1355 1360
 His Thr Ser Asp Asn Pro Phe Leu His Ser His Arg Asp Asp Gln Arg
 1365 1370 1375
 Leu Val Ile Gly Arg Cys Pro Ser Asp Pro Tyr Lys His Ser Leu Pro
 1380 1385 1390
 Ser Gln Ala Val Asn Asp Ser Tyr Leu Arg Ser Ser Leu Arg Ser Thr
 1395 1400 1405
 Ala Ser Tyr Cys Ser Arg Asp Ser Arg Gly His Asn Asp Val Tyr Ile
 1410 1415 1420
 Ser Glu His Val Met Pro Tyr Ala Ala Asn Lys Asn Asn Met Tyr Ser
 1425 1430 1435 1440
 Thr Pro Arg Val Leu Asn Ser Cys Ser Asn Arg Arg Val Tyr Lys Glu
 1445 1450 1455
 Met Pro Ser Ile Glu Ser Asp Val
 1460

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 74 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CGAGGGAGGC GGCCGGCGCG GACTCTCTTC GCGGGCGCAG CGCCCCCTTC CCCTCGGACC 60
CTCCGGTGGA CATG 74

(2) INFORMATION FOR SEQ ID NO:13:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5538 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) **FEATURE:**

- (A) NAME/KEY: CDS
(B) LOCATION: 210..4664

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

TTGAATTTGC	ATCTCTTCAA	GACACAAGAT	TAAAACAAAA	TTTACGCTAA	ATTGGATTTT	60
AAATTATCTT	CCGTTTCATTT	ATCCTTCGTC	TTTCTTATGT	GGATATGCAA	GCGAGAAGAA	120
GGGACTGGAC	ATTCCCAACA	TGCTCACTCC	CTTAATCTGT	CCGTCTAGAG	GTTTGGCTTC	180
TACAAACCAA	GGGAGTCGAC	GAGTTGAAG	ATG AAG CCC AGA GCG GAG TGC TGT			233
			Met Lys Pro Arg Ala Glu Cys Cys			
			1	5		
TCT CCC AAG TTC TGG TTG GTG TTG GCC GTC CTG GCC GTG TCA GGC AGC						281
Ser Pro Lys Phe Trp Leu Val Leu Ala Val Leu Ala Val Ser Gly Ser						
	10		15	20		
AGA GCT CGT TCT CAG AAG AGC CCC CCC AGC ATT GGC ATT GCT GTC ATC						329
Arg Ala Arg Ser Gln Lys Ser Pro Pro Ser Ile Gly Ile Ala Val Ile						
	25		30	35	40	
CTC GTG GGC ACT TCC GAC GAG GTG GCC ATC AAG GAT GCC CAC GAG AAA						377
Leu Val Gly Thr Ser Asp Glu Val Ala Ile Lys Asp Ala His Glu Lys						
	45		50	55		
GAT GAT TTC CAC CAT CTC TCC GTG GTA CCC CGG GTG GAA CTG GTA GCC						425
Asp Asp Phe His His Leu Ser Val Val Pro Arg Val Glu Leu Val Ala						
	60		65	70		
ATG AAT GAG ACC GAC CCA AAG AGC ATC ATC ACC CGC ATC TGT GAT CTC						473
Met Asn Glu Thr Asp Pro Lys Ser Ile Ile Thr Arg Ile Cys Asp Leu						
	75		80	85		
ATG TCT GAC CGG AAG ATC CAG GGG GTG GTG TTT GCT GAT GAC ACA GAC						521
Met Ser Asp Arg Lys Ile Gln Gly Val Val Phe Ala Asp Asp Thr Asp						
	90		95	100		
CAG GAA GCC ATC GCC CAG ATC CTC GAT TTC ATT TCA GCA CAG ACT CTC						569
Gln Glu Ala Ile Ala Gln Ile Leu Asp Phe Ile Ser Ala Gln Thr Leu						
	105		110	115	120	
ACC CCG ATC CTG GGC ATC CAC GGG GGC TCC TCT ATG ATA ATG GCA GAT						617
Thr Pro Ile Leu Gly Ile His Gly Gly Ser Ser Met Ile Met Ala Asp						
	125		130	135		

AAG GAT GAA TCC TCC ATG TTC TTC CAG TTT GGC CCA TCA ATT GAA CAG Lys Asp Glu Ser Ser Met Phe Phe Gln Phe Gly Pro Ser Ile Glu Gln 140 145 150	665
CAA GCT TCC GTA ATG CTC AAC ATC ATG GAA GAA TAT GAC TGG TAC ATC Gln Ala Ser Val Met Leu Asn Ile Met Glu Glu Tyr Asp Trp Tyr Ile 155 160 165	713
TTT TCT ATC GTC ACC ACC TAT TTC CCT GGC TAC CAG GAC TTT GTA AAC Phe Ser Ile Val Thr Thr Tyr Phe Pro Gly Tyr Gln Asp Phe Val Asn 170 175 180	761
AAG ATC CGC AGC ACC ATT GAG AAT AGC TTT GTG GGC TGG GAG CTA GAG Lys Ile Arg Ser Thr Ile Glu Asn Ser Phe Val Gly Trp Glu Leu Glu 185 190 195 200	809
GAG GTC CTC CTA CTG GAC ATG TCC CTG GAC GAT GGA GAT TCT AAG ATC Glu Val Leu Leu Leu Asp Met Ser Leu Asp Asp Gly Asp Ser Lys Ile 205 210 215	857
CAG AAT CAG CTC AAG AAA CTT CAA AGC CCC ATC ATT CTT CTT TAC TGT Gln Asn Gln Leu Lys Lys Leu Gln Ser Pro Ile Ile Leu Leu Tyr Cys 220 225 230	905
ACC AAG GAA GAA GCC ACC TAC ATC TTT GAA GTG GCC AAC TCA GTA GGG Thr Lys Glu Glu Ala Thr Tyr Ile Phe Glu Val Ala Asn Ser Val Gly 235 240 245	953
CTG ACT GGC TAT GGC TAC ACG TGG ATC GTG CCC AGT CTG GTG GCA GGG Leu Thr Gly Tyr Gly Tyr Thr Trp Ile Val Pro Ser Leu Val Ala Gly 250 255 260	1001
GAT ACA GAC ACA GTG CCT GCG GAG TTC CCC ACT GGG CTC ATC TCT GTA Asp Thr Asp Thr Val Pro Ala Glu Phe Pro Thr Gly Leu Ile Ser Val 265 270 275 280	1049
TCA TAT GAT GAA TGG GAC TAT GGC CTC CCC CCC AGA GTG AGA GAT GGA Ser Tyr Asp Glu Trp Asp Tyr Gly Leu Pro Pro Arg Val Arg Asp Gly 285 290 295	1097
ATT GCC ATA ATC ACC ACT GCT GCT TCT GAC ATG CTG TCT GAG CAC AGC Ile Ala Ile Ile Thr Thr Ala Ala Ser Asp Met Leu Ser Glu His Ser 300 305 310	1145
TTC ATC CCT GAG CCC AAA AGC AGT TGT TAC AAC ACC CAC GAG AAG AGA Phe Ile Pro Glu Pro Lys Ser Ser Cys Tyr Asn Thr His Glu Lys Arg 315 320 325	1193
ATC TAC CAG TCC AAT ATG CTAAAT AGG TAT CTG ATC AAT GTC ACT TTT Ile Tyr Gln Ser Asn Met Leu Asn Arg Tyr Leu Ile Asn Val Thr Phe 330 335 340	1241
GAG GGG AGG AAT TTG TCC TTC AGT GAA GAT GGC TAC CAG ATG CAC CCG Glu Gly Arg Asn Leu Ser Phe Ser Glu Asp Gly Tyr Gln Met His Pro 345 350 355 360	1289
AAA CTG GTG ATA ATT CTT CTG AAC AAG GAG AGG AAG TGG GAA AGG GTG Lys Leu Val Ile Ile Leu Leu Asn Lys Glu Arg Lys Trp Glu Arg Val 365 370 375	1337
GGG AAG TGG AAA GAC AAG TCC CTG CAG ATG AAG TAC TAT GTG TGG CCC Gly Lys Trp Lys Asp Lys Ser Leu Gln Met Lys Tyr Tyr Val Trp Pro 380 385 390	1385
CGA ATG TGT CCA GAG ACT GAA GAG CAG GAG GAT GAC CAT CTG AGC ATT Arg Met Cys Pro Glu Thr Glu Glu Gln Glu Asp Asp His Leu Ser Ile 395 400 405	1433

GTG ACC CTG GAG GAG GCA CCA TTT GTC ATT GTG GAA AGT GTG GAC CCT Val Thr Leu Glu Glu Ala Pro Phe Val Ile Val Glu Ser Val Asp Pro 410 415 420	1481
CTG AGT GGA ACC TGC ATG AGG AAC ACA GTC CCC TGC CAA AAA CGC ATA Leu Ser Gly Thr Cys Met Arg Asn Thr Val Pro Cys Gln Lys Arg Ile 425 430 435 440	1529
GTC ACT GAG AAT AAA ACA GAC GAG GAG CCG GGT TAC ATC AAA AAA TGC Val Thr Glu Asn Lys Thr Asp Glu Glu Pro Gly Tyr Ile Lys Lys Cys 445 450 455	1577
TGC AAG GGG TTC TGT ATT GAC ATC CTT AAG AAA ATT TCT AAA TCT GTG Cys Lys Gly Phe Cys Ile Asp Ile Leu Lys Lys Ile Ser Lys Ser Val 460 465 470	1625
AAG TTC ACC TAT GAC CTT TAC CTG GTT ACC AAT GGC AAG CAT GGG AAG Lys Phe Thr Tyr Asp Leu Tyr Leu Val Thr Asn Gly Lys His Gly Lys 475 480 485	1673
AAA ATC AAT GGA ACC TGG AAT GGT ATG ATT GGA GAG GTG GTC ATG AAG Lys Ile Asn Gly Thr Trp Asn Gly Met Ile Gly Glu Val Val Met Lys 490 495 500	1721
AGG GCC TAC ATG GCA GTG GGC TCA CTC ACC ATC AAT GAG GAA CGA TCG Arg Ala Tyr Met Ala Val Gly Ser Leu Thr Ile Asn Glu Glu Arg Ser 505 510 515 520	1769
GAG GTG GTC GAC TTC TCT GTG CCC TTC ATA GAG ACA GGC ATC AGT GTC Glu Val Val Asp Phe Ser Val Pro Phe Ile Glu Thr Gly Ile Ser Val 525 530 535	1817
ATG GTC TCA CGC AGC AAT GGG ACT GTC TCA CCT TCT GCC TTC TTA GAG Met Val Ser Arg Ser Asn Gly Thr Val Ser Pro Ser Ala Phe Leu Glu 540 545 550	1865
CCA TTC AGC GCT GAC GTA TGG GTG ATG ATG TTT GTG ATG CTG CTC ATC Pro Phe Ser Ala Asp Val Trp Val Met Met Phe Val Met Leu Leu Ile 555 560 565	1913
GTC TCA GCC GTG GCT GTC TTT GTC TTT GAG TAC TTC AGC CCT GTG GGT Val Ser Ala Val Ala Val Phe Val Phe Glu Tyr Phe Ser Pro Val Gly 570 575 580	1961
TAT AAC AGG TGC CTC GCT GAT GGC AGA GAG CCT GGT GGA CCC TCT TTC Tyr Asn Arg Cys Leu Ala Asp Gly Arg Glu Pro Gly Gly Pro Ser Phe 585 590 595 600	2009
ACC ATC GGC AAA GCT ATT TGG TTG CTC TGG GGT CTG GTG TTT AAC AAC Thr Ile Gly Lys Ala Ile Trp Leu Leu Trp Gly Leu Val Phe Asn Asn 605 610 615	2057
TCC GTA CCT GTG CAG AAC CCA AAG GGG ACC ACC TCC AAG ATC ATG GTG Ser Val Pro Val Gln Asn Pro Lys Gly Thr Thr Ser Lys Ile Met Val 620 625 630	2105
TCA GTG TGG GCC TTC TTT GCT GTC ATC TTC CTG GCC AGC TAC ACT GCC Ser Val Trp Ala Phe Phe Ala Val Ile Phe Leu Ala Ser Tyr Thr Ala 635 640 645	2153
AAC TTA GCT GCC TTC ATG ATC CAA GAG GAA TAT GTG GAC CAG GTT TCT Asn Leu Ala Ala Phe Met Ile Gln Glu Glu Tyr Val Asp Gln Val Ser 650 655 660	2201
GGC CTG AGC GAC AAA AAG TTC CAG AGA CCT AAT GAC TTC TCA CCC CCT Gly Leu Ser Asp Lys Lys Phe Gln Arg Pro Asn Asp Phe Ser Pro Pro 665 670 675 680	2249

TTC	CGC	TTT	GGG	ACC	GTG	CCC	AAC	GGC	AGC	ACA	GAG	AGA	AAT	ATT	CGC	2297
Phe	Arg	Phe	Gly	Thr	Val	Pro	Asn	Gly	Ser	Thr	Glu	Arg	Asn	Ile	Arg	
				685					690					695		
AAT	AAC	TAT	GCA	GAA	ATG	CAT	GCC	TAC	ATG	GGA	AAG	TTC	AAC	CAG	AGG	2345
Asn	Asn	Tyr	Ala	Glu	Met	His	Ala	Tyr	Met	Gly	Lys	Phe	Asn	Gln	Arg	
			700					705					710			
GGT	GTA	GAT	GAT	GCA	TTG	CTC	TCC	CTG	AAA	ACA	GGG	AAA	CTG	GAT	GCC	2393
Gly	Val	Asp	Asp	Ala	Leu	Leu	Ser	Leu	Lys	Thr	Gly	Lys	Leu	Asp	Ala	
		715					720					725				
TTC	ATC	TAT	GAT	GCA	GCA	GTG	CTG	AAC	TAT	ATG	GCA	GGC	AGA	GAT	GAA	2441
Phe	Ile	Tyr	Asp	Ala	Ala	Val	Leu	Asn	Tyr	Met	Ala	Gly	Arg	Asp	Glu	
	730					735					740					
GGC	TGC	AAG	CTG	GTG	ACC	ATT	GGC	AGT	GGG	AAG	GTC	TTT	GCT	TCC	ACT	2489
Gly	Cys	Lys	Leu	Val	Thr	Ile	Gly	Ser	Gly	Lys	Val	Phe	Ala	Ser	Thr	
	745				750				755						760	
GGC	TAT	GGC	ATT	GCC	ATC	CAA	AAA	GAT	TCT	GGG	TGG	AAG	CGC	CAG	GTG	2537
Gly	Tyr	Gly	Ile	Ala	Ile	Gln	Lys	Asp	Ser	Gly	Trp	Lys	Arg	Gln	Val	
				765					770					775		
GAC	CTT	GCT	ATC	CTG	CAG	CTC	TTT	GGA	GAT	GGG	GAG	ATG	GAA	GAA	CTG	2585
Asp	Leu	Ala	Ile	Leu	Gln	Leu	Phe	Gly	Asp	Gly	Glu	Met	Glu	Glu	Leu	
			780					785					790			
GAA	GCT	CTC	TGG	CTC	ACT	GGC	ATT	TGT	CAC	AAT	GAG	AAG	AAT	GAG	GTC	2633
Glu	Ala	Leu	Trp	Leu	Thr	Gly	Ile	Cys	His	Asn	Glu	Lys	Asn	Glu	Val	
		795					800					805				
ATG	AGC	AGC	CAG	CTG	GAC	ATT	GAC	AAC	ATG	GCA	GGG	GTC	TTC	TAC	ATG	2681
Met	Ser	Ser	Gln	Leu	Asp	Ile	Asp	Asn	Met	Ala	Gly	Val	Phe	Tyr	Met	
	810					815					820					
TTG	GGG	GCG	GCC	ATG	GCT	CTC	AGC	CTC	ATC	ACC	TTC	ATC	TGC	GAA	CAC	2729
Leu	Gly	Ala	Ala	Met	Ala	Leu	Ser	Leu	Ile	Thr	Phe	Ile	Cys	Glu	His	
	825				830					835					840	
CTT	TTC	TAT	TGG	CAG	TTC	CGA	CAT	TGC	TTT	ATG	GGT	GTC	TGT	TCT	GGC	2777
Leu	Phe	Tyr	Trp	Gln	Phe	Arg	His	Cys	Phe	Met	Gly	Val	Cys	Ser	Gly	
				845					850					855		
AAG	CCT	GGC	ATG	GTC	TTC	TCC	ATC	AGC	AGA	GGT	ATC	TAC	AGC	TGC	ATC	2825
Lys	Pro	Gly	Met	Val	Phe	Ser	Ile	Ser	Arg	Gly	Ile	Tyr	Ser	Cys	Ile	
			860					865					870			
CAT	GGG	GTG	GCG	ATC	GAG	GAG	CGC	CAG	TCT	GTA	ATG	AAC	TCC	CCC	ACC	2873
His	Gly	Val	Ala	Ile	Glu	Glu	Arg	Gln	Ser	Val	Met	Asn	Ser	Pro	Thr	
		875					880					885				
GCA	ACC	ATG	AAC	AAC	ACA	CAC	TCC	AAC	ATC	CTG	CGC	CTG	CTG	CGC	ACG	2921
Ala	Thr	Met	Asn	Asn	Thr	His	Ser	Asn	Ile	Leu	Arg	Leu	Leu	Arg	Thr	
	890					895					900					
GCC	AAG	AAC	ATG	GCT	AAC	CTG	TCT	GGT	GTG	AAT	GGC	TCA	CCG	CAG	AGC	2969
Ala	Lys	Asn	Met	Ala	Asn	Leu	Ser	Gly	Val	Asn	Gly	Ser	Pro	Gln	Ser	
	905				910					915					920	
GCC	CTG	GAC	TTC	ATC	CGA	CGG	GAG	TCA	TCC	GTC	TAT	GAC	ATC	TCA	GAG	3017
Ala	Leu	Asp	Phe	Ile	Arg	Arg	Glu	Ser	Ser	Val	Tyr	Asp	Ile	Ser	Glu	
				925					930					935		
CAC	CGC	CGC	AGC	TTC	ACG	CAT	TCT	GAC	TGC	AAA	TCC	TAC	AAC	AAC	CCG	3065
His	Arg	Arg	Ser	Phe	Thr	His	Ser	Asp	Cys	Lys	Ser	Tyr	Asn	Asn	Pro	
			940					945					950			

CCC	TGT	GAG	GAG	AAC	CTC	TTC	AGT	GAC	TAC	ATC	AGT	GAG	GTA	GAG	AGA	3113
Pro	Cys	Glu	Glu	Asn	Leu	Phe	Ser	Asp	Tyr	Ile	Ser	Glu	Val	Glu	Arg	
		955					960					965				
ACG	TTC	GGG	AAC	CTG	CAG	CTG	AAG	GAC	AGC	AAC	GTG	TAC	CAA	GAT	CAC	3161
Thr	Phe	Gly	Asn	Leu	Gln	Leu	Lys	Asp	Ser	Asn	Val	Tyr	Gln	Asp	His	
	970					975					980					
TAC	CAC	CAT	CAC	CAC	CGG	CCC	CAT	AGT	ATT	GGC	AGT	GCC	AGC	TCC	ATC	3209
Tyr	His	His	His	His	Arg	Pro	His	Ser	Ile	Gly	Ser	Ala	Ser	Ser	Ile	
985					990					995					1000	
GAT	GGG	CTC	TAC	GAC	TGT	GAC	AAC	CCA	CCC	TTC	ACC	ACC	CAG	TCC	AGG	3257
Asp	Gly	Leu	Tyr	Asp	Cys	Asp	Asn	Pro	Pro	Phe	Thr	Thr	Gln	Ser	Arg	
				1005					1010					1015		
TCC	ATC	AGC	AAG	AAG	CCC	CTG	GAC	ATC	GGC	CTC	CCC	TCC	TCC	AAG	CAC	3305
Ser	Ile	Ser	Lys	Lys	Pro	Leu	Asp	Ile	Gly	Leu	Pro	Ser	Ser	Lys	His	
			1020					1025					1030			
AGC	CAG	CTC	AGT	GAC	CTG	TAC	GGC	AAA	TTC	TCC	TTC	AAG	AGC	GAC	CGC	3353
Ser	Gln	Leu	Ser	Asp	Leu	Tyr	Gly	Lys	Phe	Ser	Phe	Lys	Ser	Asp	Arg	
		1035					1040					1045				
TAC	AGT	GGC	CAC	GAC	GAC	TTG	ATC	CGC	TCC	GAT	GTC	TCT	GAC	ATC	TCA	3401
Tyr	Ser	Gly	His	Asp	Asp	Leu	Ile	Arg	Ser	Asp	Val	Ser	Asp	Ile	Ser	
	1050					1055					1060					
ACC	CAC	ACC	GTC	ACC	TAT	GGG	AAC	ATC	GAG	GGC	AAT	GCC	GCC	AAG	AGG	3449
Thr	His	Thr	Val	Thr	Tyr	Gly	Asn	Ile	Glu	Gly	Asn	Ala	Ala	Lys	Arg	
1065					1070					1075					1080	
CGT	AAG	CAG	CAA	TAT	AAG	GAC	AGC	CTG	AAG	AAG	CGG	CCT	GCC	TCG	GCC	3497
Arg	Lys	Gln	Gln	Tyr	Lys	Asp	Ser	Leu	Lys	Lys	Arg	Pro	Ala	Ser	Ala	
				1085					1090					1095		
AAG	TCC	CGC	AGG	GAG	TTT	GAC	GAG	ATC	GAG	CTG	GCC	TAC	CGT	CGC	CGA	3545
Lys	Ser	Arg	Arg	Glu	Phe	Asp	Glu	Ile	Glu	Leu	Ala	Tyr	Arg	Arg	Arg	
			1100					1105					1110			
CCG	CCC	CGC	TCC	CCT	GAC	CAC	AAG	CGC	TAC	TTC	AGG	GAC	AAG	GAA	GGG	3593
Pro	Pro	Arg	Ser	Pro	Asp	His	Lys	Arg	Tyr	Phe	Arg	Asp	Lys	Glu	Gly	
		1115					1120					1125				
CTA	CGG	GAC	TTC	TAC	CTG	GAC	CAG	TTC	CGA	ACA	AAG	GAG	AAC	TCA	CCC	3641
Leu	Arg	Asp	Phe	Tyr	Leu	Asp	Gln	Phe	Arg	Thr	Lys	Glu	Asn	Ser	Pro	
	1130					1135					1140					
CAC	TGG	GAG	CAC	GTA	GAC	CTG	ACC	GAC	ATC	TAC	AAG	GAG	CGG	AGT	GAT	3689
His	Trp	Glu	His	Val	Asp	Leu	Thr	Asp	Ile	Tyr	Lys	Glu	Arg	Ser	Asp	
1145					1150					1155					1160	
GAC	TTT	AAG	CGC	GAC	TCC	ATC	AGC	GGA	GGA	GGG	CCC	TGT	ACC	AAC	AGG	3737
Asp	Phe	Lys	Arg	Asp	Ser	Ile	Ser	Gly	Gly	Gly	Pro	Cys	Thr	Asn	Arg	
				1165					1170					1175		
TCT	CAC	ATC	AAG	CAC	GGG	ACG	GGC	GAC	AAA	CAC	GGC	GTG	GTC	AGC	GGG	3785
Ser	His	Ile	Lys	His	Gly	Thr	Gly	Asp	Lys	His	Gly	Val	Val	Ser	Gly	
			1180					1185					1190			
GTA	CCT	GCA	CCT	TGG	GAG	AAG	AAC	CTG	ACC	AAC	GTG	GAG	TGG	GAG	GAC	3833
Val	Pro	Ala	Pro	Trp	Glu	Lys	Asn	Leu	Thr	Asn	Val	Glu	Trp	Glu	Asp	
		1195					1200					1205				
CGG	TCC	GGG	GGC	AAC	TTC	TGC	CGC	AGC	TGT	CCC	TCC	AAG	CTG	CAC	AAC	3881
Arg	Ser	Gly	Gly	Asn	Phe	Cys	Arg	Ser	Cys	Pro	Ser	Lys	Leu	His	Asn	
	1210					1215					1220					

TAC TCC ACG ACG GTG ACG GGT CAG AAC TCG GGC AGG CAG GCG TGC ATC Tyr Ser Thr Thr Val Thr Gly Gln Asn Ser Gly Arg Gln Ala Cys Ile 1225 1230 1235 1240	3929
CGG TGT GAG GCT TGC AAG AAA GCA GGC AAC CTG TAT GAC ATC AGT GAG Arg Cys Glu Ala Cys Lys Lys Ala Gly Asn Leu Tyr Asp Ile Ser Glu 1245 1250 1255	3977
GAC AAC TCC CTG CAG GAA CTG GAC CAG CCG GCT GCC CCA GTG GCG GTG Asp Asn Ser Leu Gln Glu Leu Asp Gln Pro Ala Ala Pro Val Ala Val 1260 1265 1270	4025
ACG TCA AAC GCC TCC ACC ACT AAG TAC CCT CAG AGC CCG ACT AAT TCC Thr Ser Asn Ala Ser Thr Thr Lys Tyr Pro Gln Ser Pro Thr Asn Ser 1275 1280 1285	4073
AAG GCC CAG AAG AAG AAC CGG AAC AAA CTG CGC CGG CAG CAC TCC TAC Lys Ala Gln Lys Lys Asn Arg Asn Lys Leu Arg Arg Gln His Ser Tyr 1290 1295 1300	4121
GAC ACC TTC GTG GAC CTG CAG AAG GAA GAA GCC GCC CTG GCC CCG CGC Asp Thr Phe Val Asp Leu Gln Lys Glu Glu Ala Ala Leu Ala Pro Arg 1305 1310 1315 1320	4169
AGC GTA AGC CTG AAA GAC AAG GGC CGA TTC ATG GAT GGG AGC CCC TAC Ser Val Ser Leu Lys Asp Lys Gly Arg Phe Met Asp Gly Ser Pro Tyr 1325 1330 1335	4217
GCC CAC ATG TTT GAG ATG TCA GCT GGC GAG AGC ACC TTT GCC AAC AAC Ala His Met Phe Glu Met Ser Ala Gly Glu Ser Thr Phe Ala Asn Asn 1340 1345 1350	4265
AAG TCC TCA GTG CCC ACT GCC GGA CAT CAC CAC CAC AAC AAC CCC GGC Lys Ser Ser Val Pro Thr Ala Gly His His His His Asn Asn Pro Gly 1355 1360 1365	4313
GGC GGG TAC ATG CTC AGC AAG TCG CTC TAC CCT GAC CGG GTC ACG CAA Gly Gly Tyr Met Leu Ser Lys Ser Leu Tyr Pro Asp Arg Val Thr Gln 1370 1375 1380	4361
AAC CCT TTC ATC CCC ACT TTT GGG GAC GAC CAG TGC TTG CTC CAT GGC Asn Pro Phe Ile Pro Thr Phe Gly Asp Asp Gln Cys Leu Leu His Gly 1385 1390 1395 1400	4409
AGC AAA TCC TAC TTC TTC AGG CAG CCC ACG GTG GCG GGG GCG TCG AAA Ser Lys Ser Tyr Phe Phe Arg Gln Pro Thr Val Ala Gly Ala Ser Lys 1405 1410 1415	4457
GCC AGG CCG GAC TTC CGG GCC CTT GTC ACC AAC AAG CCG GTG GTC TCG Ala Arg Pro Asp Phe Arg Ala Leu Val Thr Asn Lys Pro Val Val Ser 1420 1425 1430	4505
GCC CTT CAT GGG GCC GTG CCA GCC CGT TTC CAG AAG GAC ATC TGT ATA Ala Leu His Gly Ala Val Pro Ala Arg Phe Gln Lys Asp Ile Cys Ile 1435 1440 1445	4553
GGG AAC CAG TCC AAC CCC TGT GTG CCT AAC AAC ACA AAC CCC AGG GCT Gly Asn Gln Ser Asn Pro Cys Val Pro Asn Asn Thr Asn Pro Arg Ala 1450 1455 1460	4601
TTC AAT GGC TCC AGC AAT GGG CAT GTT TAT GAG AAA CTT TCT AGT ATT Phe Asn Gly Ser Ser Asn Gly His Val Tyr Glu Lys Leu Ser Ser Ile 1465 1470 1475 1480	4649
GAG TCT GAT GTC TGAGTGAGGG AACAGAGAGG TTAAGGTGGG TACGGGAGGG Glu Ser Asp Val	4701

TAAGGCTGTG GGTGCGGTGA TGCGCATGTC ACGGAGGGTG ACGGGGGTGA ACTTGGTTCC	4761
CATTTGCTCC TTTCTTGTTT TAATTTATTT ATGGGATCCT GGAGTTCTGG TTCCTACTGG	4821
GGGCAACCCT GGTGACCAGC ACCATCTCTC CTCCTTTTCA CAGTTCTCTC CTTCTTCCCC	4881
CCGCTGTCAG CCATTCTGT TCCCATGAGA TGATGCCATG GGCCCTCTCA GCAGGGGAGG	4941
GTAGAGCGGA GAAAGGAAGG GCTGCATGCG GGCTTCCTCC TGGTGTGGAA GAGCTCCTTG	5001
ATATCCTCTT TGAGTGAAGC TGGGAGAACC AAAAAGAGGC TATGTGAGCA CAAAGGTAGC	5061
TTTTCCCAA CTGATCTTTT CATTTAGGTG AGGAAGCAAA AGCATCTATG TGAGACCATT	5121
TAGCACACTG CTTGTGAAAG GAAAGAGGCT CTGGCTAAAT TCATGCTGCT TAGATGACAT	5181
CTGTCTAGGA ATCATGTGCC AAGCAGAGGT TGGGAGGCCA TTTGTGTTTA TATATAAGCC	5241
CAAAAATGCT TGCTTCAACC CCATGAGACT CGATAGTGGT GGTGAACAGA ACCCAAGGTC	5301
ATTGGTGGCA GAGTGGATTG TTGAACAAAC TGGAAAGTAC GTTATGATAG TGTCCCCGG	5361
TGCCTTGGGG ACAAGAGCAG GTGGATTGTG CGTGCATGTG TGTTTCATGCA CACTTGCACC	5421
CATGTGTAGT CAGGTGCCTC AAGAGAAGGC AACCTTGACT CTTTCGTTGA ATTTGCATCT	5481
CTTCAAGACA CAAGATTAAA ACAAATTTA CGCTAAATTG GATTTTAAAT TATCTTC	5538

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1484 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met	Lys	Pro	Arg	Ala	Glu	Cys	Cys	Ser	Pro	Lys	Phe	Trp	Leu	Val	Leu
1				5					10					15	
Ala	Val	Leu	Ala	Val	Ser	Gly	Ser	Arg	Ala	Arg	Ser	Gln	Lys	Ser	Pro
			20					25					30		
Pro	Ser	Ile	Gly	Ile	Ala	Val	Ile	Leu	Val	Gly	Thr	Ser	Asp	Glu	Val
		35					40					45			
Ala	Ile	Lys	Asp	Ala	His	Glu	Lys	Asp	Asp	Phe	His	His	Leu	Ser	Val
	50					55					60				
Val	Pro	Arg	Val	Glu	Leu	Val	Ala	Met	Asn	Glu	Thr	Asp	Pro	Lys	Ser
65				70					75					80	
Ile	Ile	Thr	Arg	Ile	Cys	Asp	Leu	Met	Ser	Asp	Arg	Lys	Ile	Gln	Gly
			85					90					95		
Val	Val	Phe	Ala	Asp	Asp	Thr	Asp	Gln	Glu	Ala	Ile	Ala	Gln	Ile	Leu
			100				105						110		
Asp	Phe	Ile	Ser	Ala	Gln	Thr	Leu	Thr	Pro	Ile	Leu	Gly	Ile	His	Gly
	115					120					125				
Gly	Ser	Ser	Met	Ile	Met	Ala	Asp	Lys	Asp	Glu	Ser	Ser	Met	Phe	Phe
130					135						140				

Gln Phe Gly Pro Ser Ile Glu Gln Gln Ala Ser Val Met Leu Asn Ile
 145 150 155 160
 Met Glu Glu Tyr Asp Trp Tyr Ile Phe Ser Ile Val Thr Thr Tyr Phe
 165 170 175
 Pro Gly Tyr Gln Asp Phe Val Asn Lys Ile Arg Ser Thr Ile Glu Asn
 180 185 190
 Ser Phe Val Gly Trp Glu Leu Glu Glu Val Leu Leu Leu Asp Met Ser
 195 200 205
 Leu Asp Asp Gly Asp Ser Lys Ile Gln Asn Gln Leu Lys Lys Leu Gln
 210 215 220
 Ser Pro Ile Ile Leu Leu Tyr Cys Thr Lys Glu Glu Ala Thr Tyr Ile
 225 230 235 240
 Phe Glu Val Ala Asn Ser Val Gly Leu Thr Gly Tyr Gly Tyr Thr Trp
 245 250 255
 Ile Val Pro Ser Leu Val Ala Gly Asp Thr Asp Thr Val Pro Ala Glu
 260 265 270
 Phe Pro Thr Gly Leu Ile Ser Val Ser Tyr Asp Glu Trp Asp Tyr Gly
 275 280 285
 Leu Pro Pro Arg Val Arg Asp Gly Ile Ala Ile Ile Thr Thr Ala Ala
 290 295 300
 Ser Asp Met Leu Ser Glu His Ser Phe Ile Pro Glu Pro Lys Ser Ser
 305 310 315 320
 Cys Tyr Asn Thr His Glu Lys Arg Ile Tyr Gln Ser Asn Met Leu Asn
 325 330 335
 Arg Tyr Leu Ile Asn Val Thr Phe Glu Gly Arg Asn Leu Ser Phe Ser
 340 345 350
 Glu Asp Gly Tyr Gln Met His Pro Lys Leu Val Ile Ile Leu Leu Asn
 355 360 365
 Lys Glu Arg Lys Trp Glu Arg Val Gly Lys Trp Lys Asp Lys Ser Leu
 370 375 380
 Gln Met Lys Tyr Tyr Val Trp Pro Arg Met Cys Pro Glu Thr Glu Glu
 385 390 395 400
 Gln Glu Asp Asp His Leu Ser Ile Val Thr Leu Glu Glu Ala Pro Phe
 405 410 415
 Val Ile Val Glu Ser Val Asp Pro Leu Ser Gly Thr Cys Met Arg Asn
 420 425 430
 Thr Val Pro Cys Gln Lys Arg Ile Val Thr Glu Asn Lys Thr Asp Glu
 435 440 445
 Glu Pro Gly Tyr Ile Lys Lys Cys Cys Lys Gly Phe Cys Ile Asp Ile
 450 455 460
 Leu Lys Lys Ile Ser Lys Ser Val Lys Phe Thr Tyr Asp Leu Tyr Leu
 465 470 475 480
 Val Thr Asn Gly Lys His Gly Lys Lys Ile Asn Gly Thr Trp Asn Gly
 485 490 495

Met Ile Gly Glu Val Val Met Lys Arg Ala Tyr Met Ala Val Gly Ser
 500 505 510
 Leu Thr Ile Asn Glu Glu Arg Ser Glu Val Val Asp Phe Ser Val Pro
 515 520 525
 Phe Ile Glu Thr Gly Ile Ser Val Me Val Ser Arg Ser Asn Gly Thr
 530 535 540
 Val Ser Pro Ser Ala Phe Leu Glu Pro Phe Ser Ala Asp Val Trp Val
 545 550 555 560
 Met Met Phe Val Met Leu Leu Ile Val Ser Ala Val Ala Val Phe Val
 565 570 575
 Phe Glu Tyr Phe Ser Pro Val Gly Tyr Asn Arg Cys Leu Ala Asp Gly
 580 585 590
 Arg Glu Pro Gly Gly Pro Ser Phe Thr Ile Gly Lys Ala Ile Trp Leu
 595 600 605
 Leu Trp Gly Leu Val Phe Asn Asn Ser Val Pro Val Gln Asn Pro Lys
 610 615 620
 Gly Thr Thr Ser Lys Ile Met Val Ser Val Trp Ala Phe Phe Ala Val
 625 630 635 640
 Ile Phe Leu Ala Ser Tyr Thr Ala Asn Leu Ala Ala Phe Met Ile Gln
 645 650 655
 Glu Glu Tyr Val Asp Gln Val Ser Gly Leu Ser Asp Lys Lys Phe Gln
 660 665 670
 Arg Pro Asn Asp Phe Ser Pro Pro Phe Arg Phe Gly Thr Val Pro Asn
 675 680 685
 Gly Ser Thr Glu Arg Asn Ile Arg Asn Asn Tyr Ala Glu Met His Ala
 690 695 700
 Tyr Met Gly Lys Phe Asn Gln Arg Gly Val Asp Asp Ala Leu Leu Ser
 705 710 715 720
 Leu Lys Thr Gly Lys Leu Asp Ala Phe Ile Tyr Asp Ala Ala Val Leu
 725 730 735
 Asn Tyr Met Ala Gly Arg Asp Glu Gly Cys Lys Leu Val Thr Ile Gly
 740 745 750
 Ser Gly Lys Val Phe Ala Ser Thr Gly Tyr Gly Ile Ala Ile Gln Lys
 755 760 765
 Asp Ser Gly Trp Lys Arg Gln Val Asp Leu Ala Ile Leu Gln Leu Phe
 770 775 780
 Gly Asp Gly Glu Met Glu Glu Leu Glu Ala Leu Trp Leu Thr Gly Ile
 785 790 795 800
 Cys His Asn Glu Lys Asn Glu Val Met Ser Ser Gln Leu Asp Ile Asp
 805 810 815
 Asn Met Ala Gly Val Phe Tyr Met Leu Gly Ala Ala Met Ala Leu Ser
 820 825 830
 Leu Ile Thr Phe Ile Cys Glu His Leu Phe Tyr Trp Gln Phe Arg His
 835 840 845

Cys Phe Met Gly Val Cys Ser Gly Lys Pro Gly Met Val Phe Ser Ile
 850 855 860
 Ser Arg Gly Ile Tyr Ser Cys Ile His Gly Val Ala Ile Glu Glu Arg
 865 870 875 880
 Gln Ser Val Met Asn Ser Pro Thr Ala Thr Met Asn Asn Thr His Ser
 885 890 895
 Asn Ile Leu Arg Leu Leu Arg Thr Ala Lys Asn Met Ala Asn Leu Ser
 900 905 910
 Gly Val Asn Gly Ser Pro Gln Ser Ala Leu Asp Phe Ile Arg Arg Glu
 915 920 925
 Ser Ser Val Tyr Asp Ile Ser Glu His Arg Arg Ser Phe Thr His Ser
 930 935 940
 Asp Cys Lys Ser Tyr Asn Asn Pro Pro Cys Glu Glu Asn Leu Phe Ser
 945 950 955 960
 Asp Tyr Ile Ser Glu Val Glu Arg Thr Phe Gly Asn Leu Gln Leu Lys
 965 970 975
 Asp Ser Asn Val Tyr Gln Asp His Tyr His His His His Arg Pro His
 980 985 990
 Ser Ile Gly Ser Ala Ser Ser Ile Asp Gly Leu Tyr Asp Cys Asp Asn
 995 1000 1005
 Pro Pro Phe Thr Thr Gln Ser Arg Ser Ile Ser Lys Lys Pro Leu Asp
 1010 1015 1020
 Ile Gly Leu Pro Ser Ser Lys His Ser Gln Leu Ser Asp Leu Tyr Gly
 1025 1030 1035 1040
 Lys Phe Ser Phe Lys Ser Asp Arg Tyr Ser Gly His Asp Asp Leu Ile
 1045 1050 1055
 Arg Ser Asp Val Ser Asp Ile Ser Thr His Thr Val Thr Tyr Gly Asn
 1060 1065 1070
 Ile Glu Gly Asn Ala Ala Lys Arg Arg Lys Gln Gln Tyr Lys Asp Ser
 1075 1080 1085
 Leu Lys Lys Arg Pro Ala Ser Ala Lys Ser Arg Arg Glu Phe Asp Glu
 1090 1095 1100
 Ile Glu Leu Ala Tyr Arg Arg Arg Pro Pro Arg Ser Pro Asp His Lys
 1105 1110 1115 1120
 Arg Tyr Phe Arg Asp Lys Glu Gly Leu Arg Asp Phe Tyr Leu Asp Gln
 1125 1130 1135
 Phe Arg Thr Lys Glu Asn Ser Pro His Trp Glu His Val Asp Leu Thr
 1140 1145 1150
 Asp Ile Tyr Lys Glu Arg Ser Asp Asp Phe Lys Arg Asp Ser Ile Ser
 1155 1160 1165
 Gly Gly Gly Pro Cys Thr Asn Arg Ser His Ile Lys His Gly Thr Gly
 1170 1175 1180
 Asp Lys His Gly Val Val Ser Gly Val Pro Ala Pro Trp Glu Lys Asn
 1185 1190 1195 1200

Leu Thr Asn Val Glu Trp Glu Asp Arg Ser Gly Gly Asn Phe Cys Arg
 1205 1210 1215
 Ser Cys Pro Ser Lys Leu His Asn Tyr Ser Thr Thr Val Thr Gly Gln
 1220 1225 1230
 Asn Ser Gly Arg Gln Ala Cys Ile Arg Cys Glu Ala Cys Lys Lys Ala
 1235 1240 1245
 Gly Asn Leu Tyr Asp Ile Ser Glu Asp Asn Ser Leu Gln Glu Leu Asp
 1250 1255 1260
 Gln Pro Ala Ala Pro Val Ala Val Thr Ser Asn Ala Ser Thr Thr Lys
 1265 1270 1275 1280
 Tyr Pro Gln Ser Pro Thr Asn Ser Lys Ala Gln Lys Lys Asn Arg Asn
 1285 1290 1295
 Lys Leu Arg Arg Gln His Ser Tyr Asp Thr Phe Val Asp Leu Gln Lys
 1300 1305 1310
 Glu Glu Ala Ala Leu Ala Pro Arg Ser Val Ser Leu Lys Asp Lys Gly
 1315 1320 1325
 Arg Phe Met Asp Gly Ser Pro Tyr Ala His Met Phe Glu Met Ser Ala
 1330 1335 1340
 Gly Glu Ser Thr Phe Ala Asn Asn Lys Ser Ser Val Pro Thr Ala Gly
 1345 1350 1355 1360
 His His His His Asn Asn Pro Gly Gly Gly Tyr Met Leu Ser Lys Ser
 1365 1370 1375
 Leu Tyr Pro Asp Arg Val Thr Gln Asn Pro Phe Ile Pro Thr Phe Gly
 1380 1385 1390
 Asp Asp Gln Cys Leu Leu His Gly Ser Lys Ser Tyr Phe Phe Arg Gln
 1395 1400 1405
 Pro Thr Val Ala Gly Ala Ser Lys Ala Arg Pro Asp Phe Arg Ala Leu
 1410 1415 1420
 Val Thr Asn Lys Pro Val Val Ser Ala Leu His Gly Ala Val Pro Ala
 1425 1430 1435 1440
 Arg Phe Gln Lys Asp Ile Cys Ile Gly Asn Gln Ser Asn Pro Cys Val
 1445 1450 1455
 Pro Asn Asn Thr Asn Pro Arg Ala Phe Asn Gly Ser Ser Asn Gly His
 1460 1465 1470
 Val Tyr Glu Lys Leu Ser Ser Ile Glu Ser Asp Val
 1475 1480

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4695 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 485..4495

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CGAGAACACA GCGAGTGTGT GAGTCCCTCC CGCTCCAGCT CCTCCAAGCC GCGGCCGCCG	60
CCGCCACCCT CGCCCGCAGC CTCCCGCAGC CTCCCTCGGC CACCGGTGTC TGGTGGGGGT	120
GTTGCCTGGG TAGGTCGGCC CGGCCCCCAG GGGTCTCTCG AGCGTCTGCC ATCTGCCCGA	180
GAAACATGTG TGGCCACGTC CTCGCCTAGT CCAGGTGGCC GCAACCTTGG GGGAGAGACA	240
GGGCAGGACA GGACCAAGGT AAGAGGTAAG GAGGAGACGG CGCCAGGGAC AGACAGGAGG	300
TCCCGGCTTG CCGTTGTGCG CACCACCACT GCCGCCGCC CGGGGCCTGC CCCCACATC	360
GGCTCTCTGA GCCCTCTCG GAATCTTGGG GTCGCTGGAC GCCGGGTTC GGTCTGGCC	420
CCCCCGCCAT CCCCCAACA GAACAGGGTC ATGAAAAGAG GCCGCCCGGC GGGGCCCGCA	480
GGCG ATG CGC GGC GCC GGT GGC CCC CGC GGC CCT CGG GGC CCC GCT AAG	529
Met Arg Gly Ala Gly Gly Pro Arg Gly Pro Arg Gly Pro Ala Lys	
1 5 10 15	
ATG CTG CTG CTG CTG GCG CTG GCC TGC GCC AGC CCG TTC CCG GAG GAG	577
Met Leu Leu Leu Leu Ala Leu Ala Cys Ser Pro Phe Pro Glu Glu	
20 25 30	
GCG CCG GGG CCG GGC GGG GCC GGT GGG CCC GGC GGC GGC CTC GGC GGG	625
Ala Pro Gly Pro Gly Gly Ala Gly Gly Pro Gly Gly Gly Leu Gly Gly	
35 40 45	
GCG CCG CCG CTC AAC GTG GCG CTC GTG TTC TCG GGG CCC GCG TAC GCG	673
Ala Arg Pro Leu Asn Val Ala Leu Val Phe Ser Gly Pro Ala Tyr Ala	
50 55 60	
GCC GAG GCG GCA CGC CTG GGC CCG GCC GTG GCG GCG GCG GTG CGC AGC	721
Ala Glu Ala Ala Arg Leu Gly Pro Ala Val Ala Ala Ala Val Arg Ser	
65 70 75	
CCG GGC CTA GAC GTG CGG CCC GTG GCG CTG GTG CTC AAC GGC TCG GAC	769
Pro Gly Leu Asp Val Arg Pro Val Ala Leu Val Leu Asn Gly Ser Asp	
80 85 90 95	
CCG CGC AGC CTC GTG CTG CAG CTC TGC GAC CTG CTG TCG GGG TTG CGC	817
Pro Arg Ser Leu Val Leu Gln Leu Cys Asp Leu Leu Ser Gly Leu Arg	
100 105 110	
GTG CAC GGC GTG GTC TTC GAA GAC GAC TCG CGC GCG CCC GCC GTC GCG	865
Val His Gly Val Val Phe Glu Asp Asp Ser Arg Ala Pro Ala Val Ala	
115 120 125	
CCC ATC CTC GAC TTC CTG TCG GCG CAG ACC TCG CTC CCC ATC GTG TCC	913
Pro Ile Leu Asp Phe Leu Ser Ala Gln Thr Ser Leu Pro Ile Val Ser	
130 135 140	
GAG CAC GGC GGC GCC GCG CTC GTG CTC ACG CCC AAG GAG AAG GGC TCC	961
Glu His Gly Gly Ala Ala Leu Val Leu Thr Pro Lys Glu Lys Gly Ser	
145 150 155	
ACC TTC CTC CAC CTG GGC TCT TCC CCC GAG CAA CAG CTT CAG GTC ATC	1009
Thr Phe Leu His Leu Gly Ser Ser Pro Glu Gln Gln Leu Gln Val Ile	
160 165 170 175	

TTT GAG GTG CTG GAG GAG TAT GAC TGG ACG TCC TTT GTA GCC GTG ACC Phe Glu Val Leu Glu Tyr Asp Trp Thr Ser Phe Val Ala Val Thr 180 185 190	1057
ACT CGT GCC CCT GGC CAC CGG GCC TTC CTG TCC TAC ATT GAG GTG CTG Thr Arg Ala Pro Gly His Arg Ala Phe Leu Ser Tyr Ile Glu Val Leu 195 200 205	1105
ACT GAC GGC AGT CTG GTG GGC TGG GAG CAC CGC GGA GCG CTG ACG CTG Thr Asp Gly Ser Leu Val Gly Trp Glu His Arg Gly Ala Leu Thr Leu 210 215 220	1153
GAC CCT GGC GCG GGC GAG GCC GTG CTC AGT GCC CAG CTC CGC AGT GTC Asp Pro Gly Ala Gly Glu Ala Val Leu Ser Ala Gln Leu Arg Ser Val 225 230 235	1201
AGC GCG CAG ATC CGC CTG CTC TTC TGC GCC CGA GAG GAG GCC GAG CCC Ser Ala Gln Ile Arg Leu Leu Phe Cys Ala Arg Glu Glu Ala Glu Pro 240 245 250 255	1249
GTG TTC CGC GCA GCT GAG GAG GCT GGC CTC ACT GGA TCT GGC TAC GTC Val Phe Arg Ala Glu Glu Ala Gly Leu Thr Gly Ser Gly Tyr Val 260 265 270	1297
TGG TTC ATG GTG GGG CCC CAG CTG GCT GGA GGC GGG GGC TCT GGG GCC Trp Phe Met Val Gly Pro Gln Leu Ala Gly Gly Gly Gly Ser Gly Ala 275 280 285	1345
CCT GGT GAG CCC CCT CTT CTG CCA GGA GGC GCC CCC CTG CCT GCC GGG Pro Gly Glu Pro Pro Leu Leu Pro Gly Gly Ala Pro Leu Pro Ala Gly 290 295 300	1393
CTG TTT GCA GTG CGC TCG GCT GGC TGG CGG GAT GAC CTG GCT CGG CGA Leu Phe Ala Val Arg Ser Ala Gly Trp Arg Asp Asp Leu Ala Arg Arg 305 310 315	1441
GTG GCA GCT GGC GTG GCC GTA GTG GCC AGA GGT GCC CAG GCC CTG CTG Val Ala Ala Gly Val Ala Val Val Ala Arg Gly Ala Gln Ala Leu Leu 320 325 330 335	1489
CGT GAT TAT GGT TTC CTT CCT GAG CTC GGC CAC GAC TGT CGC GCC CAG Arg Asp Tyr Gly Phe Leu Pro Glu Leu Gly His Asp Cys Arg Ala Gln 340 345 350	1537
AAC CGC ACC CAC CGC GGG GAG AGT CTG CAT AGG TAC TTC ATG AAC ATC Asn Arg Thr His Arg Gly Glu Ser Leu His Arg Tyr Phe Met Asn Ile 355 360 365	1585
ACG TGG GAT AAC CGG GAT TAC TCC TTC AAT GAG GAC GGC TTC CTA GTG Thr Trp Asp Asn Arg Asp Tyr Ser Phe Asn Glu Asp Gly Phe Leu Val 370 375 380	1633
AAC CCC TCC CTG GTG GTC ATC TCC CTC ACC AGA GAC AGG ACG TGG GAG Asn Pro Ser Leu Val Val Ile Ser Leu Thr Arg Asp Arg Thr Trp Glu 385 390 395	1681
GTG GTG GGC AGC TGG GAG CAG CAG ACG CTC CGC CTC AAG TAC CCG CTG Val Val Gly Ser Trp Glu Gln Gln Thr Leu Arg Leu Lys Tyr Pro Leu 400 405 410 415	1729
TGG TCC CGC TAT GGT CGC TTC CTG CAG CCA GTG GAC GAC ACG CAG CAC Trp Ser Arg Tyr Gly Arg Phe Leu Gln Pro Val Asp Asp Thr Gln His 420 425 430	1777
CTC GCG GTG GCC ACG CTG GAG GAA AGG CCG TTT GTC ATC GTG GAG CCT Leu Ala Val Ala Thr Leu Glu Glu Arg Pro Phe Val Ile Val Glu Pro 435 440 445	1825

GCA	GAC	CCT	ATC	AGC	GGC	ACC	TGC	ATC	CGA	GAC	TCC	GTC	CCC	TGC	CGG	1873
Ala	Asp	Pro	Ile	Ser	Gly	Thr	Cys	Ile	Arg	Asp	Ser	Val	Pro	Cys	Arg	
	450						455					460				
AGC	CAG	CTC	AAC	CGA	ACC	CAC	AGC	CCT	CCA	CCG	GAT	GCC	CCC	CGC	CCG	1921
Ser	Gln	Leu	Asn	Arg	Thr	His	Ser	Pro	Pro	Pro	Asp	Ala	Pro	Arg	Pro	
	465						470				475					
GAA	AAG	CGC	TGC	TGC	AAG	GGT	TTC	TGC	ATC	GAC	ATT	CTG	AAG	CGG	CTG	1969
Glu	Lys	Arg	Cys	Cys	Lys	Gly	Phe	Cys	Ile	Asp	Ile	Leu	Lys	Arg	Leu	
480					485					490					495	
GGC	CAT	ACC	ATC	GGC	TTC	AGC	TAC	GAC	CTC	TAC	CTG	GTC	ACC	AAT	GGC	2017
Ala	His	Thr	Ile	Gly	Phe	Ser	Tyr	Asp	Leu	Tyr	Leu	Val	Thr	Asn	Gly	
				500					505					510		
AAG	CAC	GGA	AAG	AAG	ATC	GAT	GGC	GTC	TGG	AAC	GGC	ATG	ATC	GGG	GAG	2065
Lys	His	Gly	Lys	Lys	Ile	Asp	Gly	Val	Trp	Asn	Gly	Met	Ile	Gly	Glu	
			515					520					525			
GTG	TTC	TAC	CAG	CGC	GCA	GAC	ATG	GCC	ATC	GGC	TCC	CTC	ACC	ATC	AAC	2113
Val	Phe	Tyr	Gln	Arg	Ala	Asp	Met	Ala	Ile	Gly	Ser	Leu	Thr	Ile	Asn	
	530						535					540				
GAG	GAG	CGC	TCC	GAG	ATC	GTG	GAC	TTC	TCC	GTC	CCC	TTC	GTG	GAG	ACC	2161
Glu	Glu	Arg	Ser	Glu	Ile	Val	Asp	Phe	Ser	Val	Pro	Phe	Val	Glu	Thr	
	545					550					555					
GGC	ATC	AGC	GTC	ATG	GTG	GCG	CGC	AGC	AAT	GGC	ACG	GTG	TCC	CCC	TCG	2209
Gly	Ile	Ser	Val	Met	Val	Ala	Arg	Ser	Asn	Gly	Thr	Val	Ser	Pro	Ser	
560					565					570					575	
GCC	TTC	CTC	GAG	CCC	TAC	AGC	CCC	GCC	GTG	TGG	GTG	ATG	ATG	TTC	GTC	2257
Ala	Phe	Leu	Glu	Pro	Tyr	Ser	Pro	Ala	Val	Trp	Val	Met	Met	Phe	Val	
				580					585					590		
ATG	TGC	CTC	ACT	GTG	GTC	GCC	GTC	ACT	GTT	TTC	ATC	TTC	GAG	TAC	CTC	2305
Met	Cys	Leu	Thr	Val	Val	Ala	Val	Thr	Val	Phe	Ile	Phe	Glu	Tyr	Leu	
			595					600					605			
AGT	CCT	GTT	GGT	TAC	AAC	CGC	AGC	CTG	GCC	ACG	GGC	AAG	CGC	CCT	GGC	2353
Ser	Pro	Val	Gly	Tyr	Asn	Arg	Ser	Leu	Ala	Thr	Gly	Lys	Arg	Pro	Gly	
	610						615					620				
GGT	TCA	ACC	TTC	ACC	ATT	GGG	AAA	TCC	ATC	TGG	CTG	CTC	TGG	GCC	CTG	2401
Gly	Ser	Thr	Phe	Thr	Ile	Gly	Lys	Ser	Ile	Trp	Leu	Leu	Trp	Ala	Leu	
	625					630					635					
GTG	TTC	AAT	AAT	TCG	GTG	CCC	GTG	GAG	AAC	CCC	CGG	GGA	ACC	ACC	AGC	2449
Val	Phe	Asn	Asn	Ser	Val	Pro	Val	Glu	Asn	Pro	Arg	Gly	Thr	Thr	Ser	
640					645					650					655	
AAA	ATC	ATG	GTG	CTG	GTG	TGG	GCC	TTC	TTC	GCC	GTC	ATC	TTC	CTC	GCC	2497
Lys	Ile	Met	Val	Leu	Val	Trp	Ala	Phe	Phe	Ala	Val	Ile	Phe	Leu	Ala	
				660				665						670		
AGC	TAC	ACA	GCC	AAC	CTG	GCC	GCC	TTC	ATG	ATC	CAG	GAG	GAG	TAC	GTG	2545
Ser	Tyr	Thr	Ala	Asn	Leu	Ala	Ala	Phe	Met	Ile	Gln	Glu	Glu	Tyr	Val	
			675					680					685			
GAT	ACT	GTG	TCT	GGG	CTC	AGT	GAC	CGC	AAG	TTC	CAG	AGG	CCC	CAG	GAG	2593
Asp	Thr	Val	Ser	Gly	Leu	Ser	Asp	Arg	Lys	Phe	Gln	Arg	Pro	Gln	Glu	
		690					695					700				
CAG	TAC	CCG	CCC	CTG	AAG	TTT	GGG	ACC	GTG	CCC	AAC	GGC	TCC	ACG	GAG	2641
Gln	Tyr	Pro	Pro	Leu	Lys	Phe	Gly	Thr	Val	Pro	Asn	Gly	Ser	Thr	Glu	
	705					710					715					

AAG Lys 720	AAC Asn	ATC Ile	CGC Arg	AGC Ser	AAC Asn 725	TAT Tyr	CCC Pro	GAC Asp	ATG Met	CAC His 730	AGC Ser	TAC Tyr	ATG Met	GTG Val	CGC Arg 735	2689
TAC Tyr	AAC Asn	CAG Gln	CCC Pro	CGC Arg 740	GTA Val	GAG Glu	GAA Glu	GCG Ala	CTC Leu 745	ACT Thr	CAG Gln	CTC Leu	AAG Lys	GCA Ala 750	GGG Gly	2737
AAG Lys	CTG Leu	GAC Asp 755	GCC Ala 755	TTC Phe	ATC Ile	TAC Tyr	GAT Asp	GCT Ala 760	GCA Ala	GTG Val	CTC Leu	AAT Asn	TAC Tyr	ATG Met	GCC Ala	2785
CGC Arg	AAG Lys 770	GAC Asp	GAG Glu	GGC Gly	TGC Cys	AAG Lys	CTT Leu 775	GTC Val	ACC Thr	ATC Ile	GGC Gly	TCC Ser	GGC Gly	AAG Lys	GTC Val	2833
TTC Phe 785	GCC Ala	ACG Thr	ACA Thr	GGC Gly	TAT Tyr	GGC Ile 790	ATC Ala	GCC Leu	CTG His	CAC Lys 795	AAG Gly	GGC Ser	TCC Arg	CGC Trp	TGG	2881
AAG Lys 800	CGG Arg	CCC Pro	ATC Ile	GAC Asp 805	CTG Leu 805	GCG Ala	TTG Leu	CTG Leu	CAG Gln	TTC Phe 810	CTG Leu	GGG Gly	GAT Asp	GAT Asp	GAG Glu 815	2929
ATC Ile	GAG Glu	ATG Met	CTG Leu	GAG Glu 820	CGG Arg	CTG Leu	TGG Trp	CTC Leu	TCT Ser 825	GGG Gly	ATC Ile	TGC Cys	CAC His	AAT Asn	GAC Asp 830	2977
AAA Lys	ATC Ile	GAG Glu	GTG Val 835	ATG Met	AGC Ser	AGC Ser	AAG Lys	CTG Leu 840	GAC Asp	ATC Ile	GAC Asp	AAC Asn	ATG Met	GCG Ala	GGC Gly	3025
GTC Val	TTC Phe	TAC Tyr	ATG Met	CTC Leu	CTG Leu	GTG Val	GCC Ala	ATG Met	GGC Gly	CTG Leu	TCC Ser	CTG Leu	CTG Leu	GTC Val	TTC Phe	3073
GCC Ala	TGG Trp 865	GAG Glu	CAC His	CTG Leu	GTG Val	TAC Tyr	TGG Trp	CGC Arg	CTG Leu	CGG Arg	CAC His	TGC Cys	CTG Leu	GGG Gly	CCC Pro	3121
ACC Thr 880	CAC His	CGC Arg	ATG Met	GAC Asp	TTC Phe	CTG Leu	CTG Leu	GCC Ala	TTC Phe	TCC Ser 890	AGG Arg	GGC Gly	ATG Met	TAC Tyr	AGC Ser 895	3169
TGC Cys	TGC Cys	AGC Ser	GCT Ala	GAG Glu 900	GCC Ala	GCC Ala	CCA Pro	CCG Pro	CCC Pro 905	GCC Ala	AAG Lys	CCC Pro	CCG Pro	CCG Pro	CCG Pro	3217
CCA Pro	CAG Gln	CCC Pro	CTG Leu 915	CCC Pro	AGC Ser	CCC Pro	GCG Ala	TAC Tyr 920	CCC Pro	GCG Ala	CCG Pro	GGG Gly	CCG Pro	GCT Ala	CCC Pro	3265
GGG Gly	CCC Pro	GCA Ala	CCT Pro	TTC Phe	GTC Val	CCC Pro	CGC Arg	GAG Glu	CGC Arg	GCC Ala	TCA Ser	GTG Val	GCC Ala	CGC Arg	TGG Trp	3313
CGC Arg	CGG Arg	CCC Pro	AAG Lys	GGC Gly	GCG Ala	GGG Gly	CCG Pro	CCG Pro	GGG Gly	GGC Gly	GCG Ala	GGC Gly	CTG Leu	GCC Ala	GAC Asp	3361
GGC Gly 960	TTC Phe	CAC His	CGC Arg	TAC Tyr	TAC Tyr	GGC Gly	CCC Pro	ATC Ile	GAG Glu	CCG Pro 970	CAG Gln	GGC Gly	CTA Leu	GGC Gly	CTC Leu 975	3409
GGC Gly	CTG Leu	GGC Gly	GAA Glu	GCG Ala	CGC Arg	GCG Ala	GCA Ala	CCG Pro	CGG Arg 985	GCG Gly	GCA Ala	GCC Ala	GGG Gly	CGC Arg	CCG Pro 990	3457

CTG TCC CCG CCG GCC GCT CAG CCC CCG CAG AAG CCG CCG GCC TCC TAT Leu Ser Pro Pro Ala Ala Gln Pro Pro Gln Lys Pro Pro Ala Ser Tyr 995 1000 1005	3505
TTC GCC ATC GTA CGC GAC AAG GAG CCA GCC GAG CCC CCC GCC GGC GCC Phe Ala Ile Val Arg Asp Lys Glu Pro Ala Glu Pro Pro Ala Gly Ala 1010 1015 1020	3553
TTC CCC GGC TTC CCG TCC CCG CCC GCG CCC CCC GCC GCC GCG GCC ACC Phe Pro Gly Phe Pro Ser Pro Pro Ala Pro Pro Ala Ala Ala Ala Thr 1025 1030 1035	3601
GCC GTC GGG CCG CCA CTC TGC CGC TTG GCC TTC GAG GAC GAG AGC CCG Ala Val Gly Pro Pro Leu Cys Arg Leu Ala Phe Glu Asp Glu Ser Pro 1040 1045 1050 1055	3649
CCG GCG CCC GCG CGG TGG CCG CGC TCG GAC CCC GAG AGC CAA CCC CTG Pro Ala Pro Ala Arg Trp Pro Arg Ser Asp Pro Glu Ser Gln Pro Leu 1060 1065 1070	3697
CTG GGG CCA GGC GCG GGC GGC GCG GGG GGC ACG GGG GGC GCA GGC GGA Leu Gly Pro Gly Ala Gly Gly Ala Gly Thr Gly Gly Ala Gly Gly 1075 1080 1085	3745
GGA GCC CCG GCC GCT CCG CCC CCG TGC TTC GCC GCG CCG CCC CCG TGC Gly Ala Pro Ala Ala Pro Pro Pro Cys Phe Ala Ala Pro Pro Pro Cys 1090 1095 1100	3793
TTT TAC CTC GAT GTC GAC CAG TCG CCG TCG GAC TCG GAG GAC TCG GAG Phe Tyr Leu Asp Val Asp Gln Ser Pro Ser Asp Ser Glu Asp Ser Glu 1105 1110 1115	3841
AGC CTG GCC GGC GCG TCC CTG GCC GGC CTG GAT CCC TGG TGG TTC GCC Ser Leu Ala Gly Ala Ser Leu Ala Gly Leu Asp Pro Trp Trp Phe Ala 1120 1125 1130 1135	3889
GAC TTC CCT TAC CCG TAT GCC GAT CGC CTC GGG CSG CCC GCG GCA CGC Asp Phe Pro Tyr Pro Tyr Ala Asp Arg Leu Gly Xaa Pro Ala Ala Arg 1140 1145 1150	3937
TAC GGA TTG GTC GAC AAA CTA GGG GGC TGG CTC GCC GGG AGC TGG GAC Tyr Gly Leu Val Asp Lys Leu Gly Gly Trp Leu Ala Gly Ser Trp Asp 1155 1160 1165	3985
TAC CTG CCT CCS CGC AGC GGT CGG GCC GCC TGG CAC TGT CCG CAC TGC Tyr Leu Pro Xaa Arg Ser Gly Arg Ala Ala Trp His Cys Arg His Cys 1170 1175 1180	4033
GCC AGC CTG GAG CTG CTT CCG CCG CCG CGC CAT CTC AGC TGC TCG CAC Ala Ser Leu Glu Leu Leu Pro Pro Pro Arg His Leu Ser Cys Ser His 1185 1190 1195	4081
GAT GGC CTG GAC GGC GGC TGG TGG GCG CCA CCG CCT CCA CCC TGG GCC Asp Gly Leu Asp Gly Gly Trp Trp Ala Pro Pro Pro Pro Trp Ala 1200 1205 1210 1215	4129
GCC GGG CCC CTG CCC CGA CGC CGG GCC CGC TGC GGG TGC CCG CGG TCG Ala Gly Pro Leu Pro Arg Arg Arg Ala Arg Cys Gly Cys Pro Arg Ser 1220 1225 1230	4177
CAC CCG CAC CGC CCG CGG GCC TCG CAC CGC ACG CCC GCC GCT GCC GCG His Pro His Arg Pro Arg Ala Ser His Arg Thr Pro Ala Ala Ala Ala 1235 1240 1245	4225
CCC CAC CAC CAC AGG CAC CGG CGC GCC GCT GGG GGC TGG GAC CTC CCG Pro His His His Arg His Arg Arg Ala Ala Gly Gly Trp Asp Leu Pro 1250 1255 1260	4273

CCG CCC GCG CCC ACC TCG CGC TCG CTC GAG GAC CTC AGC TCG TGC CCT Pro Pro Ala Pro Thr Ser Arg Ser Leu Glu Asp Leu Ser Ser Cys Pro 1265 1270 1275	4321
CGC GCC GCC CCT GCG CGC AGG CTT ACC GGG CCC TCC CGC CAC GCT CGC Arg Ala Ala Pro Ala Arg Arg Leu Thr Gly Pro Ser Arg His Ala Arg 1280 1285 1290 1295	4369
AGG TGT CCG CAC GCC GCG CAC TGG GGG CCG CCG CTG CCT ACA GCT TCC Arg Cys Pro His Ala Ala His Trp Gly Pro Pro Leu Pro Thr Ala Ser 1300 1305 1310	4417
CAC CGG AGA CAC CGG GGC GGG GAC CTG GGC ACC CGC AGG GGC TCG GCG His Arg Arg His Arg Gly Gly Asp Leu Gly Thr Arg Arg Gly Ser Ala 1315 1320 1325	4465
CAC TTC TCT AGC CTC GAG TCC GAG GTA TGACGCGGCC CCGGGGGCCC His Phe Ser Ser Leu Glu Ser Glu Val 1330 1335	4512
CACCGCCCCC TTGGTCA ^u GCG CAGGCCACGG CCCGAGGGGG CGCCCGCAGT GGACAGGACC	4572
CGCGTGGGTT GGAAGGAAA GCAGTGGAAC TGGCCGGACC CCGCCTGGAG CAGCGTCCTG	4632
CGCCCCCTGG TTCTGGAGGA ACCGCAAGCC GGAGAGGATT TGGTCCCTCA ACTATCACCC	4692
AGG	4695

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1336 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Met Arg Gly Ala Gly Gly Pro Arg Gly Pro Arg Gly Pro Ala Lys Met 1 5 10 15
Leu Leu Leu Leu Ala Leu Ala Cys Ala Ser Pro Phe Pro Glu Glu Ala 20 25 30
Pro Gly Pro Gly Gly Ala Gly Gly Pro Gly Gly Gly Leu Gly Gly Ala 35 40 45
Arg Pro Leu Asn Val Ala Leu Val Phe Ser Gly Pro Ala Tyr Ala Ala 50 55 60
Glu Ala Ala Arg Leu Gly Pro Ala Val Ala Ala Val Arg Ser Pro 65 70 75 80
Gly Leu Asp Val Arg Pro Val Ala Leu Val Leu Asn Gly Ser Asp Pro 85 90 95
Arg Ser Leu Val Leu Gln Leu Cys Asp Leu Leu Ser Gly Leu Arg Val 100 105 110
His Gly Val Val Phe Glu Asp Asp Ser Arg Ala Pro Ala Val Ala Pro 115 120 125
Ile Leu Asp Phe Leu Ser Ala Gln Thr Ser Leu Pro Ile Val Ser Glu 130 135 140

His Gly Gly Ala Ala Leu Val Leu Thr Pro Lys Glu Lys Gly Ser Thr
 145 150 155 160
 Phe Leu His Leu Gly Ser Ser Pro Glu Gln Gln Leu Gln Val Ile Phe
 165 170 175
 Glu Val Leu Glu Glu Tyr Asp Trp Thr Ser Phe Val Ala Val Thr Thr
 180 185 190
 Arg Ala Pro Gly His Arg Ala Phe Leu Ser Tyr Ile Glu Val Leu Thr
 195 200 205
 Asp Gly Ser Leu Val Gly Trp Glu His Arg Gly Ala Leu Thr Leu Asp
 210 215 220
 Pro Gly Ala Gly Glu Ala Val Leu Ser Ala Gln Leu Arg Ser Val Ser
 225 230 235 240
 Ala Gln Ile Arg Leu Leu Phe Cys Ala Arg Glu Glu Ala Glu Pro Val
 245 250 255
 Phe Arg Ala Ala Glu Glu Ala Gly Leu Thr Gly Ser Gly Tyr Val Trp
 260 265 270
 Phe Met Val Gly Pro Gln Leu Ala Gly Gly Gly Gly Ser Gly Ala Pro
 275 280 285
 Gly Glu Pro Pro Leu Leu Pro Gly Gly Ala Pro Leu Pro Ala Gly Leu
 290 295 300
 Phe Ala Val Arg Ser Ala Gly Trp Arg Asp Asp Leu Ala Arg Arg Val
 305 310 315 320
 Ala Ala Gly Val Ala Val Val Ala Arg Gly Ala Gln Ala Leu Leu Arg
 325 330 335
 Asp Tyr Gly Phe Leu Pro Glu Leu Gly His Asp Cys Arg Ala Gln Asn
 340 345 350
 Arg Thr His Arg Gly Glu Ser Leu His Arg Tyr Phe Met Asn Ile Thr
 355 360 365
 Trp Asp Asn Arg Asp Tyr Ser Phe Asn Glu Asp Gly Phe Leu Val Asn
 370 375 380
 Pro Ser Leu Val Val Ile Ser Leu Thr Arg Asp Arg Thr Trp Glu Val
 385 390 395 400
 Val Gly Ser Trp Glu Gln Gln Thr Leu Arg Leu Lys Tyr Pro Leu Trp
 405 410 415
 Ser Arg Tyr Gly Arg Phe Leu Gln Pro Val Asp Asp Thr Gln His Leu
 420 425 430
 Ala Val Ala Thr Leu Glu Glu Arg Pro Phe Val Ile Val Glu Pro Ala
 435 440 445
 Asp Pro Ile Ser Gly Thr Cys Ile Arg Asp Ser Val Pro Cys Arg Ser
 450 455 460
 Gln Leu Asn Arg Thr His Ser Pro Pro Pro Asp Ala Pro Arg Pro Glu
 465 470 475 480
 Lys Arg Cys Cys Lys Gly Phe Cys Ile Asp Ile Leu Lys Arg Leu Ala
 485 490 495

His Thr Ile Gly Phe Ser Tyr Asp Leu Tyr Leu Val Thr Asn Gly Lys
 500 505 510
 His Gly Lys Lys Ile Asp Gly Val Trp Asn Gly Met Ile Gly Glu Val
 515 520 525
 Phe Tyr Gln Arg Ala Asp Met Ala Ile Gly Ser Leu Thr Ile Asn Glu
 530 535 540
 Glu Arg Ser Glu Ile Val Asp Phe Ser Val Pro Phe Val Glu Thr Gly
 545 550 555 560
 Ile Ser Val Met Val Ala Arg Ser Asn Gly Thr Val Ser Pro Ser Ala
 565 570 575
 Phe Leu Glu Pro Tyr Ser Pro Ala Val Trp Val Met Met Phe Val Met
 580 585 590
 Cys Leu Thr Val Val Ala Val Thr Val Phe Ile Phe Glu Tyr Leu Ser
 595 600 605
 Pro Val Gly Tyr Asn Arg Ser Leu Ala Thr Gly Lys Arg Pro Gly Gly
 610 615 620
 Ser Thr Phe Thr Ile Gly Lys Ser Ile Trp Leu Leu Trp Ala Leu Val
 625 630 635 640
 Phe Asn Asn Ser Val Pro Val Glu Asn Pro Arg Gly Thr Thr Ser Lys
 645 650 655
 Ile Met Val Leu Val Trp Ala Phe Phe Ala Val Ile Phe Leu Ala Ser
 660 665 670
 Tyr Thr Ala Asn Leu Ala Ala Phe Met Ile Gln Glu Glu Tyr Val Asp
 675 680 685
 Thr Val Ser Gly Leu Ser Asp Arg Lys Phe Gln Arg Pro Gln Glu Gln
 690 695 700
 Tyr Pro Pro Leu Lys Phe Gly Thr Val Pro Asn Gly Ser Thr Glu Lys
 705 710 715 720
 Asn Ile Arg Ser Asn Tyr Pro Asp Met His Ser Tyr Met Val Arg Tyr
 725 730 735
 Asn Gln Pro Arg Val Glu Glu Ala Leu Thr Gln Leu Lys Ala Gly Lys
 740 745 750
 Leu Asp Ala Phe Ile Tyr Asp Ala Ala Val Leu Asn Tyr Met Ala Arg
 755 760 765
 Lys Asp Glu Gly Cys Lys Leu Val Thr Ile Gly Ser Gly Lys Val Phe
 770 775 780
 Ala Thr Thr Gly Tyr Gly Ile Ala Leu His Lys Gly Ser Arg Trp Lys
 785 790 795 800
 Arg Pro Ile Asp Leu Ala Leu Leu Gln Phe Leu Gly Asp Asp Glu Ile
 805 810 815
 Glu Met Leu Glu Arg Leu Trp Leu Ser Gly Ile Cys His Asn Asp Lys
 820 825 830
 Ile Glu Val Met Ser Ser Lys Leu Asp Ile Asp Asn Met Ala Gly Val
 835 840 845

Phe Tyr Met Leu Leu Val Ala Met Gly Leu Ser Leu Leu Val Phe Ala
 850 855 860
 Trp Glu His Leu Val Tyr Trp Arg Leu Arg His Cys Leu Gly Pro Thr
 865 870 875 880
 His Arg Met Asp Phe Leu Leu Ala Phe Ser Arg Gly Met Tyr Ser Cys
 885 890 895
 Cys Ser Ala Glu Ala Ala Pro Pro Pro Ala Lys Pro Pro Pro Pro Pro
 900 905 910
 Gln Pro Leu Pro Ser Pro Ala Tyr Pro Ala Pro Gly Pro Ala Pro Gly
 915 920 925
 Pro Ala Pro Phe Val Pro Arg Glu Arg Ala Ser Val Ala Arg Trp Arg
 930 935 940
 Arg Pro Lys Gly Ala Gly Pro Pro Gly Gly Ala Gly Leu Ala Asp Gly
 945 950 955 960
 Phe His Arg Tyr Tyr Gly Pro Ile Glu Pro Gln Gly Leu Gly Leu Gly
 965 970 975
 Leu Gly Glu Ala Arg Ala Ala Pro Arg Gly Ala Ala Gly Arg Pro Leu
 980 985 990
 Ser Pro Pro Ala Ala Gln Pro Pro Gln Lys Pro Pro Ala Ser Tyr Phe
 995 1000 1005
 Ala Ile Val Arg Asp Lys Glu Pro Ala Glu Pro Pro Ala Gly Ala Phe
 1010 1015 1020
 Pro Gly Phe Pro Ser Pro Pro Ala Pro Pro Ala Ala Ala Thr Ala
 1025 1030 1035 1040
 Val Gly Pro Pro Leu Cys Arg Leu Ala Phe Glu Asp Glu Ser Pro Pro
 1045 1050 1055
 Ala Pro Ala Arg Trp Pro Arg Ser Asp Pro Glu Ser Gln Pro Leu Leu
 1060 1065 1070
 Gly Pro Gly Ala Gly Gly Ala Gly Gly Thr Gly Gly Ala Gly Gly Gly
 1075 1080 1085
 Ala Pro Ala Ala Pro Pro Pro Cys Phe Ala Ala Pro Pro Pro Cys Phe
 1090 1095 1100
 Tyr Leu Asp Val Asp Gln Ser Pro Ser Asp Ser Glu Asp Ser Glu Ser
 1105 1110 1115 1120
 Leu Ala Gly Ala Ser Leu Ala Gly Leu Asp Pro Trp Trp Phe Ala Asp
 1125 1130 1135
 Phe Pro Tyr Pro Tyr Ala Asp Arg Leu Gly Xaa Pro Ala Ala Arg Tyr
 1140 1145 1150
 Gly Leu Val Asp Lys Leu Gly Gly Trp Leu Ala Gly Ser Trp Asp Tyr
 1155 1160 1165
 Leu Pro Xaa Arg Ser Gly Arg Ala Ala Trp His Cys Arg His Cys Ala
 1170 1175 1180
 Ser Leu Glu Leu Leu Pro Pro Pro Arg His Leu Ser Cys Ser His Asp
 1185 1190 1195 1200

Gly	Leu	Asp	Gly	Gly	Trp	Trp	Ala	Pro	Pro	Pro	Pro	Trp	Ala	His	
				1205									1210		
												1215			
Gly	Pro	Leu	Pro	Arg	Arg	Arg	Ala	Arg	Cys	Gly	Cys	Pro	Arg	Ser	
				1220									1225		
												1230			
Pro	His	Arg	Pro	Arg	Ala	Ser	His	Arg	Thr	Pro	Ala	Ala	Ala	Pro	
				1235									1240		
												1245			
His	His	His	Arg	His	Arg	Arg	Ala	Ala	Gly	Gly	Trp	Asp	Leu	Pro	
				1250									1255		
												1260			
Pro	Ala	Pro	Thr	Ser	Arg	Ser	Leu	Glu	Asp	Leu	Ser	Ser	Cys	Pro	
				1265									1270		
												1275			
												1280			
Ala	Ala	Pro	Ala	Arg	Arg	Leu	Thr	Gly	Pro	Ser	Arg	His	Ala	Arg	
				1285									1290		
												1295			
Cys	Pro	His	Ala	Ala	His	Trp	Gly	Pro	Pro	Leu	Pro	Thr	Ala	Ser	
				1300									1305		
												1310			
Arg	Arg	His	Arg	Gly	Gly	Asp	Leu	Gly	Thr	Arg	Arg	Gly	Ser	His	
				1315									1320		
												1325			
Phe	Ser	Ser	Leu	Glu	Ser	Glu	Val								
				1330									1335		

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GGGTGGCGGC CGCAGAGCAC CTCCACCATC TCCTTGTCCT ACTCCAAGAT CTGGCCCTAG 60
TCCATGTTTG C 71

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

TGGTGGTCCC CAACCTGTAG GACTTGGTTC TGGAGGAGGA TCTGGTGTAG GCAAACATGG 60
ACTAGGGCCA G 71

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 61 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GTTGGGGACC ACCAGATGGA GGTAGAGCTG CACTTGTACG AAGAGCTCCA CAACCACCTG 60
 G 61

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 62 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

CGTGAGACGT CAGACAAAGG AGGCCAGGT GTAGGTGGTC TACCAGGTGG TTGTGGAGCT 60
 CT 62

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 195 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

CCGCAGAGCA CCTCCACCAT CTCCTTGTC TACTCCAAGA TCTGGCCCTA GTCCATGTTT 60
 GCCTACACCA GATCCTCCTC CAGAACCAAG TCCTACAGGT TGGGGACCAC CAGATGGAGG 120
 TAGAGCTGCA CTTGTACGAA GAGCTCCACA ACCACCTGGT AGACCACCTA CACCTGGGCC 180
 TCCTTTGTCT GACGT 195